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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:05:18 ; Search time 38 Seconds
(without alignments)
1227.308 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836
Sequence: 1 MSFYSKQDYNMDELDLEYNN.....GFLNNGIKADVLNHLCHLM 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	100.0	350	22	AAE08003 Human chimeric NPY
2	1777	96.8	324	22	AAE08005 Human chimeric NPY
3	1777	96.8	394	23	ABR79512 Human chimeric neuropept
4	1743	94.9	341	22	AAE08008 Chimeric chimeric CNPY5
5	1699	92.5	341	22	AAE08014 Dog chimeric CNPY5
6	1693	92.1	383	22	AAE08009 Dog chimeric CNPY5
7	1691	92.1	352	22	AAE08011 Rat chimeric CNPY5
8	1668.5	90.9	455	17	AAE95939 Human Y5 receptor
9	1668.5	90.9	455	18	AAW29447 Human hippocampal
10	1668.5	90.9	455	18	AAW29413 Human hippocampal

11	1668.5	90.9	455	19	AAW37093 Homo sapiens hippo
12	1668.5	90.9	455	20	AAV57461 Human hippocampal
13	1668.5	90.9	455	22	AAE08002 Human neuropeptide
14	1668.5	90.9	455	23	ABR79510 Human neuropeptide
15	1665.5	90.7	455	22	AAE08016 African green monkey
16	1647	89.7	383	22	AAE08015 pig chimeric CNPY5
17	1637	89.2	355	22	AAE08013 Rat chimeric CNPY5
18	1616.5	88.0	456	19	AAW37095 Canis domesticus Y
19	1613.5	87.9	445	18	AAW27604 Human neuropeptide
20	1613.5	87.9	445	18	AAW15230 Human neuropeptide
21	1613.5	87.9	445	20	AAV14554 Human neuropeptide
22	1613.5	87.9	445	21	AAV52578 Human NPY (neurope
23	1613.5	87.9	445	22	AAE07922 Human neuropeptide
24	1613.5	87.9	445	22	AAE07958 Human neuropeptide
25	1613.5	87.9	445	22	AAE06692 Human neuropeptide
26	1613.5	87.9	445	22	AAE85110 Human neuropeptide
27	1613.5	87.9	445	22	AAE85121 Human neuropeptide
28	1610.5	87.7	445	22	AAE02851 Rhesus neuropeptid
29	1609.5	87.7	499	22	AAE08004 Human chimeric NPY
30	1604.5	87.4	445	22	Non-endogenous hum
31	1549.5	84.4	445	21	AAV52577 Chimeric rat/human
32	1536	83.7	456	17	AAE95940 Rat Y5 receptor
33	1536	83.7	456	18	AAW29446 Rat hypothalamic n
34	1536	83.7	456	18	AAW29412 Rat hypothalamic n
35	1536	83.7	456	19	AAW37092 Rattus norvegicus
36	1536	83.7	456	20	AAW37460 Rat hypothalamic Y
37	1526	83.1	445	18	AAW27603 Rat neuropeptide Y
38	1526	83.1	445	20	AAV14553 Rat neuropeptide Y
39	1526	83.1	445	21	AAV52579 Rat NPY (neuropept
40	1524	83.0	445	18	AAW15232 Rat neuropeptide Y
41	1519	82.7	445	18	AAW27602 Rat neuropeptide Y
42	1519	82.7	445	20	AAV14552 Rat neuropeptide Y
43	1511.5	82.3	466	18	AAW15233 Mouse neuropeptide
44	1482	80.7	499	22	AAE08012 Rat chimeric CNPY5
45	1461.5	79.6	508	22	AAE08010 Mouse chimeric mmp

ALIGNMENTS

RESULT 1

ID AAE08003 standard: Protein: 350 AA.

XX AAE08003:

XX

XX

XX 01-NOV-2001 (first entry)

XX

XX Human chimeric NPY5deltaY1IC3 receptor.

XX

XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;

XX Transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;

XX Huntington's disorder; Parkinson's disorder; eating disorder; seizure;

XX locomotor; anxiety disorder; limbic seizure; tranquilliser;

XX human; chimeric receptor.

XX

XX Homo sapiens.

XX

XX OS

XX

XX WO200155103-A2.

XX

XX 02-AUG-2001.

XX

XX

XX 29-JAN-2001; 2001WO-US02804.

XX

XX

XX 28-JAN-2000; 2000US-0178652.

XX

XX (NEUR-) NEUROGEN CORP.

XX

XX Bennett M, Brodbeck R, Krause J;

XX

XX WPI: 2001-514543/56.

XX

XX N-PSDB; AAD14735.

XX

Pt	New chimeric receptor proteins comprising a single polypeptide chain of amino acids, useful as targets for drug actions, and as basis for drug discovery and development -
Pt	Claim 10; Page 48-50; 72pp; English.
Pt	The present invention relates to chimeric neuropeptide Y (NPY) receptors. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY ₅ receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is human chimeric NPYSdeltaYIC3 receptor. The chimera comprises intracellular loop 3 of NPY ₅ receptor replaced with intracellular Loop 3 of NPY1 receptor.
Cc	Sequence 350 AA;
SQ	Query Match 100.0%; Score 1836; DB 22; Length 350; Best Local Similarity 100.0%; Pred. No. 5.9e-188; Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 MSFYKODYNMDELDEYYNKTLATENNNTAATRNSDPFWDDTKSSVDDLGYELIGLYNF 60
Dd	1 MSFYSKYDYMNDLEDEIYTNNKTATENNTAATRNSDPFWDDTKSSVDLDGFLLGLTYE 60
Oy	61 VSLLEGFMGNLILMALMKRKNOKTIVNFLIGNLAESDLVLVEFCSPFTLTSVLLDOMMG 120
Dd	61 VSLEFGFMGILLILMAIMKKRKNOGTIVNFLIGNLAESDLVLVEFCSPFTLTSTVLLDMGMG 120
Oy	121 KVMCHIMPLOOVSYLVSTLIISAIYKHNIKPISNNLTANGYFLIAVTWLGFI 180
Dd	121 KMVCHEMPLOOVSALYSTLIISAIRYHIKIPIHSINNLTANNGYLFAITVPWLGPXI 180
Oy	181 CSPLEVHFSLSVELQETFGSALLSRYLECVSWPSDSRYAFRTISLTVQYIIPLVCLTFYS 240
Dd	181 CSPLPVHFSLVELQETFGSALLSRYLECWSMSPOSTRAPGISLLVOYLIPVLCITYS 240
Oy	241 HTSVCIIRLKRRNMMDKARDNKTRSSRSRVFRRLTIILVFAYSMPLHLFHVVTDEND 300
Dd	241 HTSVICIRLRKRNNAMDKNDRNKTRSRSRVFFRTLIIILVFAYSMPLHLFHVVTTDEFD 300
Oy	301 NLISRHRKLNYCYICHILGMMSCCNPTILYGFLNKGIRADLVSLTHCLHM 350
Dd	301 NLISRHRKLYICYICHILGMMSCCNPTILYGFLNKGIRADVSLTHCLHM 350
Rstult_2	AEE08005
ID	AAE08005 standard; Protein; 394 AA.
Xx	AAE08005;
Xx	01-NOV-2001 (first entry)
Dt	Human chimeric NPYSdeltaYIC3/deltaYICT receptor.
Kw	Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein; Transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy; Huntington's disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser; human; chimeric receptor.
Oo	Homo sapiens.
Nn	WO200155103-A2.
Xx	02-Aug-2001.

Query Match	96.8%;	Score 1777;	DB 22;	Length 394;
Best Local Similarity	99.4%;	Pred. No. 1.4e-181;		
Matches 339;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1 MSFYISKODNMDLEDEYVKNKTLPATENNPAATRNSDFPVDDYKSSVDDLOYLGLGTYE 60	XX			
DB 1 MSFYISKODNMDLEDEYVKNKTLPATENNPAATRNSDFPVDDYKSSVDDLOYLGLGTYE 60	XX			
QY 61 VSLLEGFMGNLLTLMALMKRRNQKTVNFTLGNLAFSDDLVLVFCSPFTLTSVLLDQWFG 120	XX			
DB 61 VSLLEGFMGNLLTLMALMKRRNQKTVNFTLGNLAFSDDLVLVFCSPFTLTSVLLDQWFG 120	XX			
QY 121 KVMCHIMPELOCVSVLVSTLLISTAIYVYHMIKPIISNNLTANHGXYELIAVWTLGFAI 180	XX			
DB 121 KVMCHIMPELOCVSVLVSTLLISTAIYVYHMIKPIISNNLTANHGXYELIAVWTLGFAI 180	XX			
QY 181 CSPRLPVHSLVLEQETFGSALLSRYLCVESPSPDSYRIAFITISLLVQYIILPVCLTVS 240	XX			
DB 181 CSPRLPVHSLVLEQETFGSALLSRYLCVESPSPDSYRIAFITISLLVQYIILPVCLTVS 240	XX			
QY 241 HTSVICIRLKRNNMMDKMDKNTKRSRSRSVYRLLTILLVFAVSMPLAHLFHYVTDEND 300	XX			
DB 241 HTSVICIRLKRNNMMDKMDKNTKRSRSRSVYRLLTILLVFAVSMPLAHLFHYVTDEND 300	XX			
QY 301 NLISNRHFKLVYCIChLGLGMSCCLNPILYGFLLNNGIKRADL 341	XX			
DB 301 NLISNRHFKLVYCIChLGLGMSCCLNPILYGFLLNNGIQDRL 341	XX			
RESULT 3				
ID ABB79512				
AC ABB79512;				
DT 23-SEP-2002 (first entry)				
XX Chimeric neuropeptide receptor hNPY5deltaY1IC3/deltaY1CT.				
XX				

KM Neuropeptide Y5; NPY; NPY5; NPY1; receptor; antagonist; anorectic;
KM antiinflammatory; nootropic; neuroprotective; cardiovascular;
KM hypotensive; antidiabetic; psychiatric; anticonvulsant; caediant;
KM neuroprotective; antidepressant; haemostatic; tranquillizer;
KM neuroleptic; analgesic; antianalgesic; nephrotoxic; uropathic;
KM gastrointestinal; antiaslathmic; human; hnpysdeltayl1C3/deltayl1CT.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200246152-A2.
XX
PD 20-JUN-2002.
XX
PF 11-DEC-2001; 2001WO-US47863.
XX
PR 12-DEC-2000; 2000US-254990P.
XX
PA (NEUR-) NEUROGEN CORP.
XX
PI Bakhtavachalam R, Blum CA, Brielmann HL, Darrow JW, De Lombaert S;
PI Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;
XX
XX WPI; 2002-547845/58.
DR N-PSDB; ABBN84260.
XX
XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or
PT 3H-spiro(isobenzofuran-1,4'-piperidine; useful for treating, e.g. eating
PT disorder, psychiatric, cardiovascular disorder or diabetes -
XX
XX Example 675; Page 134; 134pp; English.
XX
XX The present sequence is the protein sequence for chimeric human
CC neuropeptide receptor hnpysdeltayl1C3/deltayl1CT, stated to comprise
CC the N-terminal amino acids 1-442 of the human neuropeptide Y5 (NPY5)
CC receptor and the C-terminal amino acids 328-384 of the human NPY1
CC receptor. The recombinant chimeric receptor was produced in Sf9
CC cells using a baculovirus expression vector. It was used to assay
CC the binding activity of compounds of the invention. Substituted
CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and
CC 3H-spiro(isobenzofuran-1,4'-piperidines capable of modulating NPY5
CC receptor activity are provided. Such compounds may be used to
CC modulate ligand binding to NPY5 receptors in vivo or in vitro,
CC and are particularly useful in the treatment of a variety of
CC disorders, e.g. eating disorders such as obesity or bulimia,
CC psychiatric disorders, diabetes and cardiovascular disorders such
CC as hypertension, in humans and animals.
XX
XX
SQ Sequence 394 AA:
Query Match 96.8%; Score 1777; DB 23; Length 394;
Best Local Similarity 99.4%; Pred. No. 1.4e-181;
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 MSFYSKODYWMDLEDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTF 60
DB 1 MSFYSKODYWMDLEDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTF 60
OY 61 VSLGFGNGLIIMALKKRNKQTVNFIIGNAFSDILVYLCSPPTLTVSLDDOMFG 120
DB 61 VSLGFGNGLIIMALKKRNKQTVNFIIGNAFSDILVYLCSPPTLTVSLDDOMFG 120
OY 121 KWCHIMPFLOCYVSLVSTLILISIAIVRYHMKHPISNNLTANHGFLATYWTGFAI 180
DB 121 KWCHIMPFLOCYVSLVSTLILISIAIVRYHMKHPISNNLTANHGFLATYWTGFAI 180
OY 181 CSPLPVFHSLEVELQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSLEVELQETFGSALLSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVS 240
OY 241 HTSVCIIRLKRNNMMKMRNKRSSRSVYFRLTLLILVFAVSMPPLHFFHYVTDFND 300
DB 241 HTSVCIIRLKRNNMMKMRNKRSSRSVYFRLTLLILVFAVSMPPLHFFHYVTDFND 300

OY 301 NLISNRHFKLYVCICHLGMMSCCLNPILYGLNNGIKADL 341
DB 301 NLISNRHFKLYVCICHLGMMSCCLNPILYGLNNGIKADL 341
RESULT 4
AAE08008
ID AAE08008 standard; Protein: 341 AA.
XX
AC AAE08008;
XX
DT 01-NOV-2001 (first entry)
XX
DE Dog chimeric cnpysdeltayl1C3 receptor.
XX
KM Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KM transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KM Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KM locomotor; anxiety disorder; limbic seizure; tranquilliser;
XX
XX dog; chimeric receptor.
XX
OS Canis sp.
XX
XX WO200155103-A2.
XX
PN 02-AUG-2001.
XX
PD 29-JAN-2001; 2001WO-US02804.
XX
PF 28-JAN-2000; 2000US-0178652.
XX
PR (NEUR-) NEUROGEN CORP.
XX
PA Bennett M, Brodbeck R, Krause J;
PI WPI; 2001-514543/56.
XX
XX New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
PT discovery and development -
XX
XX Example 2; Page 58-59; 72pp; English.
XX
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with
CC seven membrane spanning transmembrane (TM) domains. The compounds that
CC modulate the activity of a NPY receptor is useful in the preparation of
CC a medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in
CC the control of limbic seizures. The present sequence is dog chimeric
CC cnpysdeltayl1C3 receptor. The chimera comprises intracellular
CC loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
CC receptor.
XX
XX
SQ Sequence 341 AA:
Query Match 94.9%; Score 1743; DB 22; Length 341;
Best Local Similarity 97.6%; Pred. No. 5.2e-178;
Matches 332; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 11 MDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTVSLLGFGNGL 70
DB 11 MDELDEYNYKTLATENNATRNSDPPVDDYKSSVDDIQLYFLIGLYTVSLLGFGNGL 70
OY 71 LILMALKKRNKQTVNFIIGNAFSDILVYLCSPPTLTVSLDDOMFGKCHIMPF 130
DB 71 LILMALKKRNKQTVNFIIGNAFSDILVYLCSPPTLTVSLDDOMFGKCHIMPF 130
OY 131 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFLATYWTGFAICSPLPVHSL 190

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Db 121 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 180
QY 191 VELOETFGSALLSSRYLCVESMPDSYRIAFETISLLVQYILLPVCLTVSHTSVICIRLKR 250
Db 181 VELOETFGSALLSSRYLCVESMPDSYRIAFETISLLVQYILLPVCLTVSHTSVICIRLKR 240
QY 251 RNNMMDKMRDNKYSSRSRSVFYRLTILLVFAVSWMPLHFFHYVTFDNDMLISNRHEKL 310
Db 241 RNNMMDKMRDNKYSSRSRSVFYRLTILLVFAVSWMPLHFFHYVTFDNDMLISNRHEKL 300
QY 311 VYCICHLGMMSCCLNPILYGLFNNGIKADLVSLIHCHLM 350
Db 301 VYCICHLGMMSCCLNPILYGLFNNGIKADLVSLIHCHLM 340

RESULT 5
AAE08014
ID AAE08014 standard; Protein: 341 AA.
AC AAE08014;
DT 01-NOV-2001 (first entry)
XX
XX Pig chimeric pNPY5deltapyl1C3 receptor.
DE
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic seizure; tranquilliser;
KW pig; chimeric receptor.
XX
XX Cavia sp.
OS
XX WO200155103-A2.
XX
XX 02-AUG-2001.
PD
XX 29-JAN-2001; 2001WO-US02804.
PF
XX 28-JAN-2000; 2000US-0178652.
PR
XX (NEUR-) NEUROGEN CORP.
PA
XX Bennett M, Brodbeck R, Krause J;
PI
XX WPI; 2001-514543/56.
DR
XX New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
XX discovery and development -
XX
XX Example 2; Page 67-68; 72pp; English.
XX
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with
CC seven membrane spanning transmembrane (TM) domains. The compounds that
CC modulate the activity of a NPY receptor is useful in the preparation of
CC a medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in
CC the control of limbic seizures. The present sequence is pig chimeric
CC pNPY5deltapyl1C3 receptor. The chimera comprises intracellular
CC loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
CC receptor.
XX
XX Sequence 341 AA;
SQ
Query Match 92.5%; Score 1699; DB 22; Length 341;
Best Local Similarity 94.1%; Pred. No. 2,7e-173;
Matches 320; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

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QY 11 MDLEIDEXYNTLATENNNTAATRNSPDPVDDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70
Db 1 MGSEIPDYNNKTLASENTVATRNNGSPFWMEDYKGSVDLDQYFLIGLYTFVSLGFMGNL 60
QY 71 LILNAAKMRNOKTIVNFIQNLAFSDLLVLFCSPFLLTIVLDDQWFGVKCHIMEFL 130
Db 61 LILNAAKMRNOKTIVNFIQNLAFSDLLVLFCSPFLLTIVLDDQWFGVKCHIMEFL 120
QY 131 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 190
Db 121 QCVSYLSTLLISLAIRYMIKHPISNNLTANHGYFLITVMTLGFALCSPLVPHSL 180
QY 191 VELOETFGSALLSSRYLCVESMPDSYRIAFETISLLVQYILLPVCLTVSHTSVICIRLKR 250
Db 181 VELOETFGSALLSSRYLCVESMPDSYRIAFETISLLVQYILLPVCLTVSHTSVICIRLKR 240
QY 251 RNNMMDKMRDNKYSSRSRSVFYRLTILLVFAVSWMPLHFFHYVTFDNDMLISNRHEKL 310
Db 241 RNNMMDKMRDNKYSSRSRSVFYRLTILLVFAVSWMPLHFFHYVTFDNDMLISNRHEKL 300
QY 311 VYCICHLGMMSCCLNPILYGLFNNGIKADLVSLIHCHLM 350
Db 301 VYCICHLGMMSCCLNPILYGLFNNGIKADLVSLIHCHLM 340

RESULT 6
AAE08009
ID AAE08009 standard; Protein: 383 AA.
AC AAE08009;
DT 01-NOV-2001 (first entry)
XX
XX Dog chimeric cNPY5deltapyl1C3/deltapyl1C2 receptor.
DE
XX
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic seizure; tranquilliser;
KW dog; chimeric receptor.
XX
XX Canis sp.
OS
XX WO200155103-A2.
XX
XX 02-AUG-2001.
PD
XX 29-JAN-2001; 2001WO-US02804.
PF
XX 28-JAN-2000; 2000US-0178652.
PR
XX (NEUR-) NEUROGEN CORP.
PA
XX Bennett M, Brodbeck R, Krause J;
PI
XX WPI; 2001-514543/56.
DR
XX New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
XX discovery and development -
XX
XX Example 2; Page 59-60; 72pp; English.
XX
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with
CC seven membrane spanning transmembrane (TM) domains. The compounds that
CC modulate the activity of a NPY receptor is useful in the preparation of
CC a medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in

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CC the control of limbic seizures. The present sequence is a dog chimeric
 CC cnpv5delta11c3/delta1c1CT receptor. The chimera comprises
 CC intracellular loop 3 and C-terminal intracellular domain of NPY5 receptor
 CC replaced with intracellular loop 3 and C-terminal intracellular domain
 CC respectively, of NPY1 receptor.

XX
 SQ Sequence 383 AA:

Query Match 92.2%; Score 1693; DB 22; Length 383;
 Best Local Similarity 97.6%; Pred. No. 1.4e-172;
 Matches 323; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 MDLELDYNTKTATENNATATNSDFPVWDYKSSVDLDQYFLGLGYTFVSLGFGNLT 70
 ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MDLELDYNTKTATENNATATNSDFPVWDYKSSVDLDQYFLGLGYTFVSLGFGNLT 60
 QY 71 LILMALMKRNOKTYTNVFLGNLAFSDIIVLVFCSPFTLTVSLDDMMFGKVMCHIMPEL 130
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 LILMALMKRNOKTYTNVFLGNLAFSDIIVLVFCSPFTLTVSLDDMMFGKVMCHIMPEL 120
 QY 131 QCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPVPHSL 190
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 QCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPVPHSL 180
 QY 191 VELQETFGSALLSRYLCVESMPDSYRIAFITSLIYOYILPLVCLTVSHTSVCIRLKR 250
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 181 VELQETFGSALLSRYLCVESMPDSYRIAFITSLIYOYILPLVCLTVSHTSVCIRLKR 240
 QY 251 RNMMDMRNKRKTSRSRSRVFRLTLLVFAVSMPLHLFHVYDFNDNLISNRHFKL 310
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 241 RNMMDMRNKRKTSRSRSRVFRLTLLVFAVSMPLHLFHVYDFNDNLISNRHFKL 300
 QY 311 VVCICHLGMMSCCLNPILYGFNLNGIKADL 341
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 301 VVCICHLGMMSCCLNPILYGFNLNGIKADL 331

RESULT 7
 AAE08011
 ID AAE08011 standard; Protein; 352 AA.

XX
 AC AAE08011;

DT 01-NOV-2001 (first entry)

XX
 DE Rat chimeric rNPY5delta1c1c3 receptor.

XX
 KW Neuropeptide Y, NPY receptor; G-protein-coupled transmembrane protein;
 KW Transmembrane; TM domain; therapy: Obesity; blood pressure; epilepsy;
 KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
 KW locomotor; anxiety disorder; limbic seizure; tranquiliser;
 KW rat; chimeric receptor.

XX
 OS Rattus sp.

XX
 PN WO200155103-A2.

XX
 PD 02-AUG-2001.

XX
 PF 29-JAN-2001: 2001WO-US02804.

XX
 PR 28-JAN-2000: 2000US-0178652.

XX
 PA (NEUR-) NEUROGEN CORP.

XX
 PI Bennett M, Brodbeck R, Krause J;

XX
 DR WPI; 2001-514543/56.

XX
 PT New chimeric receptor proteins comprising a single polypeptide chain of
 PT amino acids, useful as targets for drug actions, and as basis for drug
 PT discovery and development
 XX

PS Example 2; Page 62-63; 72pp; English.

XX
 CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.
 CC The NPY receptors are G-protein-coupled transmembrane proteins with
 CC seven membrane spanning transmembrane (TM) domains. The compounds that
 CC modulate the activity of a NPY receptor is useful in the preparation of
 CC a medicament for treating conditions including obesity, high/low blood
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
 CC seizure, locomotor and anxiety disorders. They can also be used as
 CC targets for drug actions, and as basis for drug discovery and
 CC development. The NPY5 receptor may have an anti-epileptic activity in
 CC the control of limbic seizures. The present sequence is rat chimeric
 CC cnpv5delta1c1c3 receptor. The chimera comprises intracellular
 CC loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
 CC receptor.

XX
 SQ Sequence 352 AA:

Query Match 92.1%; Score 1691; DB 22; Length 352;
 Best Local Similarity 92.4%; Pred. No. 2e-172;
 Matches 318; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 7 QDYNMDLELDYNTKTATENNATATNSDFPVWDYKSSVDLDQYFLGLGYTFVSLGFG 66
 || :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 8 QDSSMEFKLEHFNKTFYENNTAAARNAPAMEDYRGSDVDLDQYFLGLGYTFVSLGFG 67
 QY 67 MGNLILIMALKRNOKTYTNVFLGNLAFSDIIVLVFCSPFTLTVSLDDMMFGKVMCH 126
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 68 MGNLILIMALKRNOKTYTNVFLGNLAFSDIIVLVFCSPFTLTVSLDDMMFGKVMCH 127
 QY 127 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPV 186
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 128 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFFLATVWTGFAICSPLPV 187
 QY 187 FHSVLVEKTEFGSALLSRYLCVESMPDSYRIAFITSLIYOYILPLVCLTVSHTSVCI 246
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 188 FHSVLVEKTEFGSALLSRYLCVESMPDSYRIAFITSLIYOYILPLVCLTVSHTSVCI 247
 QY 247 RLRNRNMMDMRNKRKTSRSRSRVFRLTLLVFAVSMPLHLFHVYDFNDNLISNR 306
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 248 RLRNRNMMDMRNKRKTSRSRSRVFRLTLLVFAVSMPLHLFHVYDFNDNLISNR 307
 QY 307 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADLVSLHCLHM 350
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 308 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADLVSLHCLHM 351

RESULT 8
 AAR95939
 ID AAR95939 standard; Protein; 455 AA.

XX
 AC AAR95939;

DT 14-OCT-1996 (first entry)

XX
 DE Human Y5 receptor.

XX
 KW Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;
 KW G protein-coupled receptor; agonist; antagonist; obesity;
 KW bulimia; anorexia; transgenic animal.

XX
 OS Homo sapiens.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Domain 51..77 /label= I

FT Domain 88..110 /note= "Transmembrane domain I"

FT Domain 126..147 /label= II

FT Domain 126..147 /note= "Transmembrane domain II"

FT Domain 126..147 /label= III

FT Domain 126..147 /note= "Transmembrane domain III"

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FT  Domain 166..187
FT  /label= IV
FT  /note= "transmembrane domain IV"
FT  Domain 220..242
FT  /label= V
FT  /note= "transmembrane domain V"
FT  Domain 380..403
FT  /label= VI
FT  /note= "transmembrane domain VI"
FT  Domain 416..438
FT  /label= VII
FT  /note= "transmembrane domain VII"
XX  MO9616542-A1.
XX  06-JUN-1996.
XX  01-DEC-1995; 95MO-US15646.
XX  02-DEC-1994; 94US-0349025.
XX  (SYNA-) SYNAPTIC PHARM CORP.
XX  Branchek T, Gerald CPG, Walker MM, Weinschank RL;
XX  WPI; 1996-277371/28.
XX  N-PSDB: AAT30433.
XX  Modifying feeding behaviour using Y5 receptor (ant)agonists -
XX  increases or decreases food consumption, for treatment of e.g.
XX  obesity or bulimia
XX  Claim 51; Fig 6; 235pp; English.
XX  Human hippocampal Y5 receptor (AAR95939) was identified as the
XX  homologue of rat hypothalamic Y5 receptor (AAR95940), isolated
XX  as an 'atypical Y1 receptor'. The receptor belongs to the G
XX  protein-coupled receptor superfamily. It is encoded by a cDNA
XX  clone (see also AAT30433) that was isolated from a hippocampus cDNA
XX  library using rat Y5 receptor cDNA as probe. Recombinant rat Y5
XX  receptor can be produced in prokaryotic or eukaryotic (e.g. COS,
XX  293 or Sf9 insect) host cells. It is used to identify Y5 ligands
XX  (agonists and antagonists) that can be used to treat obesity,
XX  bulimia or anorexia, and to raise monoclonal antibodies useful in
XX  detecting Y5 receptor.
XX  Sequence 455 AA;
XX  SQ
XX  Query Match 90.9%; Score 1668.5; DB 17; Length 455;
XX  Best Local Similarity 73.2%; Pred. No. 7.3e-170;
XX  Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
XX  1 MSFYSKODYNMDLELDYNNKTATENNNTATRNSDPFWDDYKSSVDDIQLYGLTYF 60
XX  1 MSFYSKODYNMDLELDYNNKTATENNNTATRNSDPFWDDYKSSVDDIQLYGLTYF 60
XX  61 VSLIGFNGNLLIIMALKKRNOQKTTVNLGNLAFSDILVVLFCSPPTLTSVLLDQWNG 120
XX  61 VSLIGFNGNLLIIMALKKRNOQKTTVNLGNLAFSDILVVLFCSPPTLTSVLLDQWNG 120
XX  61 VSLIGFNGNLLIIMALKKRNOQKTTVNLGNLAFSDILVVLFCSPPTLTSVLLDQWNG 120
XX  121 KYMHIMPFLOCVSVLSTLLISAIYRYMIMKPISSNNLTANHGFLLATVTLGFAI 180
XX  121 KYMHIMPFLOCVSVLSTLLISAIYRYMIMKPISSNNLTANHGFLLATVTLGFAI 180
XX  121 KYMHIMPFLOCVSVLSTLLISAIYRYMIMKPISSNNLTANHGFLLATVTLGFAI 180
XX  181 CSPLPVHSLVELOETFGSALISRYLCVESWPSDSYRIAFITISLLVOYTLPLVCLTVS 240
XX  181 CSPLPVHSLVELOETFGSALISRYLCVESWPSDSYRIAFITISLLVOYTLPLVCLTVS 240
XX  241 HTSVC---IRLKRNNMMDK----- 257
XX  241 HTSVCRSISGSLSKENRLEENEMINLTLHPSKSGPOVKLSGSKMSYSFIKKHRRYS 300
XX  258 -----MRDKRYR----- 264

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Db 301 KKTACVLPAPERPSQENSRILPENFGSVRSQSSKFIQVPTCEIKPEENSDVHEL 360
Oy 265 -----SSRSRSVFRLITLLIVFAVSWMPHLFHVVDNDNLISNHFPLKYVIC 315
Db 361 RYKRSVTRIKKRSRVSFRLITLLIVFAVSWMPHLFHVVDNDNLISNHFPLKYVIC 420
Oy 316 HLLGMSCCLNPILYGLFNLNGIKADLVSLIHLCLHM 350
Db 421 HLLGMSCCLNPILYGLFNLNGIKADLVSLIHLCLHM 455
XX  RESULT 9
XX  AAW29447
XX  ID AAW29447 standard; Protein: 455 AA.
XX  AC AAW29447;
XX  XX 26-FEB-1998 (first entry)
XX  DE Human hippocampal neuropeptide Y Y5 receptor.
XX  KW Hippocampal; neuropeptide Y Y5 receptor; NPY Y5; antagonist;
XX  KW epileptic seizure; migraine; sleep disturbance; propylaxis;
XX  KW eating disorder; quinzolin-2,4-diazirine.
XX  OS Homo sapiens.
XX  PN W09720822-A1.
XX  PD 12-JUN-1997.
XX  PF 18-NOV-1996; 96MO-EP05066.
XX  PR 01-DEC-1995; 95US-0566027.
XX  (NOVS ) NOVARTIS AG.
XX  PA Criscione L, Rigollier P, Rueger H, Schilling W;
XX  PI Schmidlin T, Tintelnor-blomley M, Yamaguchi Y;
XX  PI Tintelnor-blomley M;
XX  DR WPI; 1997-319712/29.
XX  N-PSDB: AAT89114.
XX  Use of new and known quinzolin-2,4-diazirine compounds as NPY Y5
XX  receptor antagonists - for treating and preventing eating disorders,
XX  diabetes, dyslipidaemia, hypertension, memory loss, epileptic
XX  seizures, migraine, sleep disturbance, etc
XX  PS Disclosure; Pages 127-129; 155pp; English.
XX  XX
XX  The present sequence represents human hippocampal neuropeptide
XX  (NP) Y receptor subtype Y5, with a pharmacological function associated
XX  with for example, obesity and eating disorders. The specification relates
XX  to a method of treatment and prophylaxis of disorders and diseases
XX  associated with with NPY receptor subtype Y5 comprising administering to
XX  a warm-blooded animal, including man, in need of such treatment a
XX  therapeutically effective amount of a quinzolin-2,4-diazirine
XX  compound. These disorders and diseases include e.g. eating disorders,
XX  obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory
XX  loss, epileptic seizures, migraine, sleep disturbance, pain,
XX  sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,
XX  shock, congestive heart failure, nasal congestion or diarrhoea.
XX  SQ
XX  Sequence 455 AA;
XX  Query Match 90.9%; Score 1668.5; DB 18; Length 455;
XX  Best Local Similarity 73.2%; Pred. No. 7.3e-170;
XX  Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
XX  1 MSFYSKODYNMDLELDYNNKTATENNNTATRNSDPFWDDYKSSVDDIQLYGLTYF 60
XX  1 MSFYSKODYNMDLELDYNNKTATENNNTATRNSDPFWDDYKSSVDDIQLYGLTYF 60

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Db 1 MSFYSKODYNMDELDEYKTKLATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
QY 61 VSLGFMGNLLIIMALKKRNOKTQTVNFIIGNLAFSDILVLFCSPTLTSLVLDQMFG 120
61 VSLGFMGNLLIIMALKKRNOKTQTVNFIIGNLAFSDILVLFCSPTLTSLVLDQMFG 120
QY 121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
Db 121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
QY 181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
Db 181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMDK----- 257
241 HTSVC-----IRLKRNNMMDK----- 257
Db 241 HTSVC-----IRLKRNNMMDK----- 257
QY 258 -----MRDKYR----- 264
258 -----MRDKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
QY 265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 315
265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 315
Db 361 RKRSVYTRIKRBSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 420
QY 316 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 350
421 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455
Db 421 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 10
AAM29413
ID AAM29413 standard; Protein; 455 AA.
XX
AC AAM29413;
XX
DT 24-FEB-1998 (first entry)
XX
DE Human hippocampal neuropeptide Y Y5 receptor.
XX
KW Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;
KW bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;
KW epileptic seizure; migraine; sleep disturbance; pain; depression;
KW sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;
KW congestive heart failure; eating disorder; obesity.
XX
OS Homo sapiens.
XX
PN MO9720820-A1.
XX
PD 12-JUN-1997.
XX
PF 18-NOV-1996; 96MO-EP05055.
XX
PR 01-DEC-1995; 95US-0566349.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Crisstone L, Rigollier P, Rueger H, Schilling W;
PI Schmidtlin T, Tintelnot-Biomley M, Yamaguchi Y;
DR WPI; 1997-319711/29.
DR N-PSDB; AAT89110.
XX
OS use of new and known heteroaryl compounds as NPY Y5-receptor
PT antagonists - for treating and preventing eating disorders,
PT diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
PT migraine, etc.
XX
PS Disclosure; Pages 76-78; 155pp; English.
XX
CC This sequence represents human hippocampal neuropeptide (NP) Y receptor
```

```
CC subtype Y5, with a pharmacological function associated with for example,
CC obesity and eating disorders. The specification relates to a method of
CC treatment and prophylaxis of disorders and diseases associated with
CC NPY receptor subtype Y5 comprising administering to a warm-blooded
CC animal, including man, in need of such treatment a therapeutically
CC effective amount of a new heteroaryl compound. These disorders and
CC diseases include e.g. eating disorders, obesity, bulimia nervosa,
CC diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
CC migraine, sleep disturbance, pain, sexual/reproductive disorders,
CC depression, anxiety, cerebral haemorrhage, shock, congestive heart
CC failure, nasal congestion or diarrhoea.
XX
SQ Sequence 455 AA:
XX
Query Match 90.9%; Score 1668.5; DB 18; Length 455;
Best Local Similarity 73.2%; Pred. No. 7.3e-170;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 1 MSFYSKODYNMDELDEYKTKLATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
1 MSFYSKODYNMDELDEYKTKLATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
Db 1 MSFYSKODYNMDELDEYKTKLATENNATATNSDPFVWDYKSSVDDIQLYFLIGLYTF 60
QY 61 VSLGFMGNLLIIMALKKRNOKTQTVNFIIGNLAFSDILVLFCSPTLTSLVLDQMFG 120
61 VSLGFMGNLLIIMALKKRNOKTQTVNFIIGNLAFSDILVLFCSPTLTSLVLDQMFG 120
Db 61 VSLGFMGNLLIIMALKKRNOKTQTVNFIIGNLAFSDILVLFCSPTLTSLVLDQMFG 120
QY 121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
Db 121 KVMCHIMPFLOQCVSVLSTLILISIAVRYHMIKHPISNNLTANHGFLATWTGFAI 180
QY 181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
Db 181 CSPLPVPHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMDK----- 257
241 HTSVC-----IRLKRNNMMDK----- 257
Db 241 HTSVC-----IRLKRNNMMDK----- 257
QY 258 -----MRDKYR----- 264
258 -----MRDKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRIIPENFGSVRSQSSSKFIQVPTCFEIKPEENSVDVHEL 360
QY 265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 315
265 -----SSRSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 315
Db 361 RKRSVYTRIKRBSRSVRYRLTILILVFAVSMPLHLFHVTTDFNDNLISNRHFKLYVCIC 420
QY 316 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 350
421 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455
Db 421 HLLGMMSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 11
AAM37093
ID AAM37093 standard; Protein; 455 AA.
XX
AC AAM37093;
XX
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens hippocampal Y5 receptor.
XX
KW Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;
KW feeding behaviour; modification; atypical neuropeptide.
XX
OS Homo sapiens.
XX
PN MO9746250-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97MO-US09504.
XX
PR 21-FEB-1997; 97US-0803600.
```


Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIIPGVPCTCEIKPEENSDVHEL 360
QY 265 -----SSRSRSVFRYLITILVFAVSMPLHLFHVYTDENDNLISNRHFKLVYCIC 315
Db 361 RVRKSVTRIKRRSRVSFRYLITILVFAVSMPLHLFHVYTDENDNLISNRHFKLVYCIC 420
QY 316 HLLGMSSCCLNPILYGFLNGIKADLVSLIHCLHM 350
Db 421 HLLGMSSCCLNPILYGFLNGIKADLVSLIHCLHM 455
RESULT 13
AAE08002
ID AAE08002 standard; Protein; 455 AA.
AC AAE08002;
XX
XX
DT 01-NOV-2001 (first entry)
XX
XX
DE Human neuropeptide Y5 (NPY5) receptor.
XX
XX
KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KM locomotor; anxiety disorder; limbic seizure; tranquilliser; human.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Domain 1..50
FT Domain /note= "N-terminal extracellular domain"
FT Domain 51..71
FT Domain /note= "First TM domain"
FT Domain 72..84
FT Domain /note= "First intracellular loop domain"
FT Domain 85..105
FT Domain /note= "Second TM domain"
FT Domain 106..125
FT Domain /note= "First extracellular loop domain"
FT Domain 126..146
FT Domain /note= "Third TM domain"
FT Domain 147..167
FT Domain /note= "Second intracellular loop domain"
FT Domain 168..188
FT Domain /note= "Fourth TM domain"
FT Domain 189..220
FT Domain /note= "Second extracellular loop domain"
FT Domain 221..241
FT Domain /note= "Fifth TM domain"
FT Domain 242..378
FT Domain /note= "Third intracellular loop domain"
FT Domain 379..401
FT Domain /note= "Sixth TM domain"
FT Domain 402..414
FT Domain /note= "Third extracellular loop domain"
FT Domain 415..438
FT Domain /note= "Seventh TM domain"
FT Domain 439..455
FT Domain /note= "C-terminal intracellular domain"
XX
XX
PN W0200155103-A2.
XX
XX
PD 02-AUG-2001.
XX
XX
PF 29-JAN-2001; 2001WO-US02804.
XX
XX
PR 28-JAN-2000; 2000US-0178652.
XX
XX
PA (NEUR-) NEUROGEN CORP.
XX
XX
PI Bennett M, Brodbeck R, Krause J;
XX
XX
DR WPI; 2001-514543/56.

DR N-PSDB; AAD14734.
XX
XX
PT New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
PT discovery and development -
XX
XX
PS Example 2; Page 55-56; 72pp; English.
XX
XX
CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with
CC seven membrane spanning transmembrane (TM) domains. The compounds that
CC modulate the activity of a NPY receptor is useful in the preparation of
CC a medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in
CC the control of limbic seizures. The present sequence is human NPY5
CC receptor.
XX
XX
SQ Sequence 455 AA;
Query Match 90.9%; Score 1668.5; DB 22; Length 455;
Best Local Similarity 73.2%; Pred. No. 7.3e-170;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 1 MSFYSKODYNMDELDEYVYKTLATENNATATRNSPFPVMDYKSSVDDQLQYFLIGLYTF 60
Db 1 MSFYSKODYNMDELDEYVYKTLATENNATATRNSPFPVMDYKSSVDDQLQYFLIGLYTF 60
QY 61 VSLIGFNGNLLIMALKKRNQKTYVNFILGNLAFSDILVLFCSPTLTSVLLDQMFEG 120
Db 61 VSLIGFNGNLLIMALKKRNQKTYVNFILGNLAFSDILVLFCSPTLTSVLLDQMFEG 120
QY 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFELATVWTGFAI 180
Db 121 KVMCHIMPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGFELATVWTGFAI 180
QY 181 CSPLPVFHSLVELQETFGSALLSRYLCVSWPSDSYRIAFITSLLYOYLPLVCLTVS 240
Db 181 CSPLPVFHSLVELQETFGSALLSRYLCVSWPSDSYRIAFITSLLYOYLPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMDK----- 257
Db 241 HTSVCRSISCCLSNKRERLEENEMINLTLPKSKSGPOVYLSGSHRWYSFIKKHRRYS 300
QY 258 -----MRDNKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIIPGVPCTCEIKPEENSDVHEL 360
QY 265 -----SSRSRSVFRYLITILVFAVSMPLHLFHVYTDENDNLISNRHFKLVYCIC 315
Db 361 RVRKSVTRIKRRSRVSFRYLITILVFAVSMPLHLFHVYTDENDNLISNRHFKLVYCIC 420
QY 316 HLLGMSSCCLNPILYGFLNGIKADLVSLIHCLHM 350
Db 421 HLLGMSSCCLNPILYGFLNGIKADLVSLIHCLHM 455
RESULT 14
ABB79510
ID ABB79510 standard; Protein; 455 AA.
XX
XX
AC ABB79510;
XX
XX
DT 23-SEP-2002 (first entry)
XX
XX
DE Human neuropeptide Y5 receptor.
XX
XX
KW Neuropeptide Y5; NPY; NPY5; receptor; human; antagonist; anorectic;
antiinflammatory; nootropic; neuroprotective; cardiovascular;
hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiac;
cerebroprotective; antidepressant; haemostatic; tranquillizer;
KW

```
KM neuroleptic; analgesic; antidiagonal; nephrotoxic; uropathic;
KW gastrointestinal; antisthmatic.
XX Homo sapiens.
XX MO200248152-A2.
XX 20-JUN-2002.
XX 11-DEC-2001; 2001WO-US47863.
XX 12-DEC-2000; 2000US-254990P.
XX (NEUR-) NEUROGEN CORP.
XX Baktavatchalam R, Blum CA, Brielmann HL, Darrow JM, De Lombaert S;
PI Hutchinson A, Tran J, Zheng X, Elliott RL, Hammond M;
XX WPI; 2002-547845/58.
XX DR N-PSDB; ABN84252.
XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or
PT 3H-spiroisobenzofuran-1,4'-piperidine, useful for treating, e.g. eating
PT disorder, psychiatric, cardiovascular disorder or diabetes.
XX Example 675; Page 129-130; 134pp; English.
XX PS
XX CC The present sequence is the protein sequence for the human
CC neuropeptide Y5 (NPY5) receptor. In an example from the
CC invention, chimeric receptors including human NPY5 receptor
CC sequences were constructed, and used to assay the binding
CC activity of compounds of the invention. Substituted
CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and
CC 3H-spiroisobenzofuran-1,4'-piperidines capable of modulating NPY5
CC receptor activity are provided. Such compounds may be used to
CC modulate ligand binding to NPY5 receptors in vivo or in vitro,
CC and are particularly useful in the treatment of a variety of
CC disorders, e.g. eating disorders such as obesity or bulimia,
CC psychiatric disorders, diabetes and cardiovascular disorders such
CC as hypertension, in humans and animals.
XX CC
XX Sequence 455 AA;
SQ
Query Match 90.9%; Score 1668.5; DB 23; Length 455;
Best Local Similarity 73.2%; Pred. No. 7.3e-170;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
OY 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60
DB 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60
OY 61 VSLGFGNGLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSLVLDQWMEG 120
DB 61 VSLGFGNGLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSLVLDQWMEG 120
OY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180
DB 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180
OY 181 CSPLPVHSLVELOETFGSALISRYLCVSPSPDSYRIATISLLVQYTLPLVCULTVS 240
DB 181 CSPLPVHSLVELOETFGSALISRYLCVSPSPDSYRIATISLLVQYTLPLVCULTVS 240
OY 241 HTSYVC---IRLKRNNMMDK----- 257
DB 241 HTSYVCIRSLGSLSKKRLDENEMINLTLHPSSKSGPOVKLSGSHKKSYSFIKKHRRYS 300
OY 258 -----MRDNKYR----- 264
DB 301 KKTACVLPADPERPSQENHSHILPENFGSVRSQSSSKFTPGVPTCEIKPEENSDVHEL 360
OY 265 -----SSRSRSVYRLTLITLIFAVSWMPHLHFNVTDFRDNLTISNRHKLVCIC 315
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DB 361 RVKRSVTRIKKRSRSVEYRLTILIFAVSWMPHLHFNVTDFRDNLTISNRHKLVCIC 420
OY 316 HLIGMSSCLNPILYGFNLNGIKADLYSLHCLHM 350
DB 421 HLIGMSSCLNPILYGFNLNGIKADLYSLHCLHM 455
RESULT 15
AAE08016
ID AAE08016 standard; Protein; 455 AA.
AC AAE08016;
DT 01-NOV-2001 (first entry)
XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.
XX DE
XX KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic seizure; tranquilliser;
KW african green monkey; AGM.
XX OS Cercopithecus aethiops.
XX PN MO200155103-A2.
XX PD 02-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US02804.
XX PR 28-JAN-2000; 2000US-0178652.
XX PA (NEUR-) NEUROGEN CORP.
XX PI Bennett M, Brodbeck R, Krause J;
XX WPI; 2001-514543/56.
XX DR N-PSDB; AAD14746.
XX PT New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
PT discovery and development.
XX PS Example 2; Page 70-72; 72pp; English.
XX PS
XX CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with
CC seven membrane spanning transmembrane (TM) domains. The compounds that
CC modulate the activity of a NPY receptor is useful in the preparation of
CC a medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in
CC the control of limbic seizures. The present sequence is african green
CC monkey (AGM) NPY5 receptor.
XX CC
XX Sequence 455 AA;
SQ
Query Match 90.7%; Score 1665.5; DB 22; Length 455;
Best Local Similarity 73.0%; Pred. No. 1.5e-169;
Matches 332; Conservative 7; Mismatches 11; Indels 105; Gaps 3;
OY 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60
DB 1 MSFYSKODYNMDELDELYNKTATENNATATRSDFPVWDYKSSVDDIQLYFLIGLYTF 60
OY 61 VSLGFGNGLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSLVLDQWMEG 120
DB 61 VSLGFGNGLILMALKKRNQKTTVNFILGNLAFSDILVLFCSPTLTSLVLDQWMEG 120
OY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180
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Db 121 KVMCHMPFLOCVSVLSTLILSLIAIARYHMIKHPISNNLTANHGFLATVWTLGPAI 180
QY 181 CSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY 241 HTSYC---IRLKRNNMMDK----- 257
Db 241 HTSYCRSISCGLSNKENRELEENEMINLHPSRKIGPOVKLSGSHKWSYSFIKKHRRYS 300
QY 258 -----MRDNKRYR----- 264
Db 301 KKTACVLPAPERBSQENHSKILPENFGSVRSQSSSKFIQVPTCFEIKPENSDVHEL 360
QY 265 -----SSRSRSVFYRLTILILVFAVSWMPLLFHVVTDFENDNLISNRHFKLYYCIC 315
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLLFHVVTDFENDNLISNRHFKLYYCIC 420
QY 316 HLLGMMSCCLNPILYGFLLNGIGKADVSLIHCLHM 350
Db 421 HLLGMMSCCLNPILYGFLLNGIGKADVSLIHCLHM 455

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Search completed: November 22, 2002, 13:09:24
 Job time : 40 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:09 ; Search time 34 Seconds
(without alignments)
2121.073 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1 MSFYSKQDYNMDELDEYTN.....GLLNGIKADLVSLHCLHM 350

Sequence: 1 MSFYSKQDYNMDELDEYTN.....GLLNGIKADLVSLHCLHM 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_minc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1610.5	87.7	445	6	09GK73
2	1589.5	86.6	446	11	09GK73
3	1219	86.4	443	13	08GFM2
4	644	35.1	383	6	09GK75
5	630	34.3	385	13	08GFM1
6	617.5	33.6	377	13	073733
7	578	31.5	377	13	08GFM3
8	554.5	30.2	374	13	08GFM3
9	539	29.4	375	13	09YHX1
10	531	28.9	375	13	057463
11	518.5	28.2	365	13	08UWV7
12	515.5	28.1	373	13	097505
13	512	27.9	372	11	073734
14	503	27.4	381	11	0922D4
15	443.5	24.2	481	5	0967T7
16	443.5	24.2	485	5	08S235

17	429	23.4	600	5	09VW75	09VW75 drosophila
18	415.5	22.6	475	5	09VW75	09VW75 drosophila
19	409	22.3	452	5	09VW75	09VW75 drosophila
20	401	21.8	290	4	099463	099463 homo sapien
21	395	21.5	336	5	09Y073	09Y073 lymnaea sta
22	389	21.2	402	5	0964E5	0964E5 dugesia tig
23	381	20.8	405	11	0924N0	0924N0 mus musculu
24	378	20.6	465	5	044426	044426 lymnaea sta
25	377.5	20.6	417	11	0924H0	0924H0 mus musculu
26	375	20.4	540	5	09VW75	09VW75 drosophila
27	374	20.4	408	4	096RV1	096RV1 homo sapien
28	370	20.2	429	5	092045	092045 lymnaea sta
29	368.5	20.1	422	11	08VHD7	08VHD7 rattus norv
30	366.5	19.9	432	11	0924G9	0924G9 rattus norv
31	366	19.9	430	4	096RN3	096RN3 homo sapien
32	362	19.7	412	5	020275	020275 caenorhabd
33	358.5	19.5	436	11	08VCC7	08VCC7 mus musculu
34	357	19.4	365	5	09XXU4	09XXU4 caenorhabd
35	355.5	19.4	436	11	09DBV6	09DBV6 mus musculu
36	346.5	18.9	397	5	09NRA4	09NRA4 boophilus m
37	345.5	18.8	399	5	020067	020067 periplaneta
38	344	18.7	423	5	0964D4	0964D4 periplaneta
39	342.5	18.7	431	5	08TBD1	08TBD1 urechis uni
40	341	18.6	357	5	09NRC8	09NRC8 drosophila
41	340.5	18.5	391	5	09GZG8	09GZG8 caenorhabd
42	335	18.2	394	4	090721	090721 drosophila
43	334	18.2	398	4	09UDE6	09UDE6 homo sapien
44	333	18.1	329	5	09VAV0	09VAV0 drosophila
45	332	18.1	361	5	08WPA2	08WPA2 bombyx mori

ALIGNMENTS

RESULT 1

09GK73 PRELIMINARY: PRT: 445 AA.

AC 09GK73;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Neuropeptide Y receptor Y5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21184974; PubMed-11287088;
RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
RA Gackenhelmer S., Johnson D., Beavers L.S., Gadsd R.A., Baez M.;
RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor
subtypes(1).";
RL Peptides 22:343-350(2001).
DR EMBL; AF303091; AAC40773.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; GPCR_Rhodopsn.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SSOURCE 445 AA; 50812 MW; AEDACD259675BC93 CRC64;

Query Match 87.7%; Score 1610.5; DB 6; Length 445;

Best Local Similarity 72.4%; Pred. No. 1.4e-128;

Matches 32; Conservative 7; Mismatches 11; Indels 105; Gaps 3;

QY 11 MDLELDYNNKTLATENNATRNSPVWDYKSSVDDQYFLGLTYTEVSLGFWGNTL 70
Db 1 MDLELDYNNKTLATENNATRNSPVWDYKSSVDDQYFLGLTYTEVSLGFWGNTL 60
OY 71 LILMALKKRNOKTTFVFLGNLAFLSILVVLVLCSPPTLISVLLDMMFKKWKCHIMPEL 130

Db 61 L1MALMKRRNQKTTVNFLIGNLAFSDILVYLFCSPTLTSVLLDQMMFGKVMCHIMPEL 120
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCSPLEPVHSL 190
Db 121 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCSPLEPVHSL 180
Qy 191 VELOETFGSALLSSRYLCVESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVC-----I 246
Db 181 VELOETFGSALLSSRYLCVESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVCISIC 240
Qy 247 RLKRRNNMADR----- 257
Db 241 GLSNKENLEENEMINLTHPSRKIGPOVKLSGSHKWSYFPIKKIRRYSKKTACVLPAP 300
Qy 258 ---MRDNKYR-----S 265
Db 301 ERPSOENHSRIIPENFGSVRSQISSSKFIPGVPTCFEIKPENSDVHELKRVKSVTRIK 360
Qy 266 SRSRSVFRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 325
Db 361 KRSRSVFRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 420
Qy 326 NPILYGFLLNGIKADLVSLIHCLHM 350
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 2

Q925F1 PRELIMINARY; PRT; 446 AA.
ID 0925F1
AC 0925F1
DT 01-DEC-2001 (TReMBUrel. 19, Created)
DT 01-DEC-2001 (TReMBUrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBUrel. 20, Last annotation update)
DE NPY receptor 5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Hystriognathii; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184976; PubMed=11287090;
RA Lundell T., Eriksson H., Marklund U., Larhammar D.;
RT "Cloning and characterization of the guinea pig neuropeptide Y
RT receptor Y5.";
RL Peptides 22:357-363(2001).
DR EMBL: AF363240; AAK52800.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;

Query Match 86.6%; Score 1589.5; DB 11; Length 446;
Best Local Similarity 71.5%; Pred. No. 8.6e-127;

Matches 318; Conservative 9; Mismatches 13; Indels 105; Gaps 3;

Qy 11 MDLEDEYNNKTATENNATATNSDPVWDYKSSVDDIYFLIGLYTFVSLGFMGNL 70
Db 1 MDLELKEYNNKTATENNATATNSDPVWDYKSSVDDIYFLIGLYTFVSLGFMGNL 60
Qy 71 L1MALMKRRNQKTTVNFLIGNLAFSDILVYLFCSPTLTSVLLDQMMFGKVMCHIMPEL 130
Db 61 L1MALMKRRNQKTTVNFLIGNLAFSDILVYLFCSPTLTSVLLDQMMFGKVMCHIMPEL 120
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCSPLEPVHSL 190
Db 121 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCSPLEPVHSL 180
Qy 191 VELOETFGSALLSSRYLCVESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVC----- 245
Db 181 VELOETFGSALLSSRYLCVESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVCISIC 240

Qy 246 -----IRL-----KRRNNMADRDNKYRSS----- 266
Db 241 GLSNKENLEENEMINLTHPSKKGQVKLSKTHKWSYFTRKRRRYSKKTACVLPAP 300
Qy 267 ----- 266
Db 301 ARPSLENSRILPENFGSVRSQISSSKFIPGVPTCFEIKPENSDAHEMRVKSITRIK 360
Qy 267 -RSRSVFRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 325
Db 361 KRSRSVFRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCCL 420
Qy 326 NPILYGFLLNGIKADLVSLIHCLHM 350
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 3

Q8QFM2 PRELIMINARY; PRT; 443 AA.
ID 08QFM2
AC 08QFM2
DT 01-JUN-2002 (TReMBUrel. 21, Created)
DT 01-JUN-2002 (TReMBUrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBUrel. 21, Last annotation update)
DE Neuropeptide Y receptor Y5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Holmberg S.K.S., Mätkö S., Boswell T., Zoorob R., Larhammar D.;
RT "Pharmacological characterization of cloned chicken neuropeptide Y
RT receptors Y1 and Y5.";
RL J. Neurochem. 81:462-471(2002).
DR EMBL: AY040844; AAK83556.1; -.
KW Receptor.
SQ SEQUENCE 443 AA; 50044 MW; EPE9F1A391CC092E CRC64;

Query Match 66.4%; Score 1219; DB 13; Length 443;
Best Local Similarity 55.5%; Pred. No. 2.1e-95;

Matches 246; Conservative 35; Mismatches 52; Indels 110; Gaps 6;

Qy 11 MDLEDEYNNKTATENNATATNSDPVWDYKSSVDDIYFLIGLYTFVSLGFMGNL 70
Db 1 MDLGFQYDNTNT-PTKNTSATTKN--FSAMEDYSSVDDIYFLIGLYTLLISLAGFYGNL 57
Qy 71 L1MALMKRRNQKTTVNFLIGNLAFSDILVYLFCSPTLTSVLLDQMMFGKVMCHIMPEL 130
Db 58 LVLTAL-TKRQKTIINILIGNLAFSDILVYLFCSPTLTSVLLDQMMFGKVMCHIMPEL 116
Qy 131 QCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCSPLEPVHSL 190
Db 117 QCVSVLSTLLISIAIVRYHMIRKVPPLSSNLTANHGFLIATVMTLGFALCSPLEPVHSL 176
Qy 191 VELOETFGSALLSSRYLCVESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVCIRLKR 250
Db 177 VDLKRTLLENLEMRRLCIESWPSDYSRIAFITISLLVQYILPLVCLTVSHTSVCISYGS 236
Qy 251 R-----NNMD----- 256
Db 237 RLSSKEGFOENEMINLTHPSKSAGTEADQPSHTSMSCALVRKHRRYSKKTSTVMPAI 296
Qy 257 ---KMRDNKYR----- 264
Db 297 LRQOQADAFDRLPPTSGTEKSSQSSSSKFIPOVPICEMRPEENTEIOMITVSQSIIRI 356
Qy 265 SRSRSVFRLTLLIVFAVSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCC 324
Db 357 KTRRRRYFCRLTYLLIVFGSWMPHLFHVYTDNFNDNLISNRHFKLYVCICHLGMMSCC 416
Qy 325 LNPILYGFLLNGIKADLVSLIHCLHM 347

```
Db 417 LNPLIGFLNNSTKADLMSLIPC 439

RESULT 4
09GK75 PRELIMINARY; PRT; 383 AA.
ID 09GK75;
AC 09GK75;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Neuropeptide Y receptor Y1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxId=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184974; PubMed=11287088;
RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
RA Gackenheim S., Johnson D., Beavers L.S., Gadsdi R.A., Baez M.;
RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor
RT subtypes(1).";
RL Reptiles 22:343-350(2001).
EMBL: AF303089; AAG40771.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPR_FL_1; UNKNOWN_1.
DR PROSITE: PS0202; G_PROTEIN_RECPR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 383 AA; 44306 MW; F872C45AA90DF62A CRC64;

Query Match 35.1%; Score 644; DB 6; Length 383;
Best Local Similarity 37.9%; Pred. No. 1e-46;
Matches 130; Conservative 70; Mismatches 122; Indels 21; Gaps 5;

QY 3 FYSKODYNMDLEDEYYNKTATENNTAATRNSDPFWDDYKSSVDDLYQYFLIGL-YTFV 61
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 6 FSGVENHVSANFSEKNAQLAFEND-----DCHLPL-----AMFTLALAGAV 50
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 62 SLGFGNLLIIMAKKRKOKTTVFLIGNLAFSDILVVFCSPTFLTSVLLDQWNGK 121
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 51 IILGVSQNLALIIILKOKEMRVNTILVNLSEFSDILVIMCLPFTFYVTLMDHWFG 110
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 122 VMCHIMPELOCVSVLSTLLISAIYRYMHKIPISNNLTANHGYFLITVWTLGFAIC 181
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 111 AMKKNLPVOCVSIIVSIFSLVLAVERHOLITNPGMRNNRHAIVGLAVIVL-AVA 168
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 182 SPLPVFHSVLQETFGSALLSS---RYLCVESMPSPDSYRIAFITISLLVQYILPVCLT 238
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 169 SSPLFLVQWTEDFQNVTLDAVKDKYVCFDQFPDSHRLSTLTLLVQYIGPLCFIF 228
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 239 VSHTSVCIRLKRNNMMDKRNKKYSSRSRFFYRTLLILVFAVSWMPHLFHVYTD 288
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 229 ICYFKYIRLKRNNMMDKRNKKYSSSETKRINIMLSIVAFAVCMPLTLTFNVEFW 288
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 299 NDMLISNRHFLVYCICHLGMSCCNPLITLGEFLNNGIADL 341
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 289 NHQIATCNHNLFLCHLTAIAMIATVCPNPLFYGLNKNFORDL 331
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 5
08QFM1 PRELIMINARY; PRT; 385 AA.
ID 08QFM1;
AC 08QFM1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Neuropeptide Y receptor Y1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Holmberg S.K.S., Mikko S., Boswell T., Zorob R., Larhammar D.;
RT "Pharmacological characterization of cloned chicken neuropeptide Y
RT receptors Y1 and Y5.";
RL J. Neurochem. 81:462-471(2002).
DR EMBL: AY040845; AAK83557.1; -.
KW Receptor.
SQ SEQUENCE 385 AA; 44365 MW; DBAA905C89D3AE84 CRC64;

Query Match 34.3%; Score 630; DB 13; Length 385;
Best Local Similarity 37.8%; Pred. No. 1.5e-45;
Matches 122; Conservative 69; Mismatches 124; Indels 8; Gaps 4;

QY 33 RNSDFPYWDYKSSVDDLYQYFLIGL-YTFVSLGFGNLLIIMAKKRKOKTTVFLIG 91
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 21 KNSOILQFEDEDCHVPLAMVFLTALAGTVIILGVSQNLALIIILKOKEMRVNTILIV 80
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 92 NLAFSDILVVFCSPTFLTSVLLDQWNGKVMCHIMPELOCVSVLSTLLISAIYRYH 151
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 81 NLSEFSDLVITMCLPFTFYVTLMDHWTFGEAMCKLNPFVOCASITVSFSLVLAIBHQ 140
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 152 MIKHPISNNLTANHGYFLITVWTLGFAICSPLPVFHSVLQETFGSALL---SSRYLC 208
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 141 LITNPGMRNNRHAIVGLAVIVLWATASSLPLFIYVLVD--EPFNIYFDEYKDKYVC 198
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 209 VESMPSPDSYRIAFITISLLVQYILPVCLTVSHTSVCIRLKRNNMMDKRNKKYSSRS 268
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 199 LDFLEPLDARLSTYTLTLVQYIGPLCFIFICYLKIYFRLKRKSNMMDKRNKYSSE 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 269 RSVEYRFLTILVFAVSWMPHLFHVYTDENML--ISNRHFLVYCICHLGMSCCN 326
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 259 KRINIMLISIVFAVCMPLTLTFNIFEDMNHILPVATCSHNLFLCHLTAIISTCVN 318
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 327 PILYGLNNGIKADLVSLINCLH 349
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 319 PIFYGLNKNFORDLQFLPFHCH 341
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 6
073733 PRELIMINARY; PRT; 377 AA.
ID 073733;
AC 073733;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Neuropeptide Y/peptide Y receptor Ya.
GN NPYRYA OR NPYRYA.
Brachydanio rerio (zebrafish) (zebra danio).
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98068842; PubMed=9407007;
RA Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuropeptide Y receptor
RT subtype in the zebrafish.";
RL DNA Cell Biol. 16:1357-1363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98096393; PubMed=9434780;
RA Ringvall M., Berglund M.M., Larhammar D.;
RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT subtype in the zebrafish.";
RL Biochem. Res. Commun. 241:749-755(1997).
RN [3]
RP SEQUENCE FROM N.A.
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RX MEDLINE-99337783;
 RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,
 RA Waith A., Soderberg C., Postlethwait J.H., Larhammar D.;
 RT "Neuropeptide y receptor subtype with unique properties cloned in the
 RT zebrafish: the zya receptor";
 RL Brain Res. Mol. Brain Res. 70:242-252(1999).
 DR EMBL: AF037400; AAC41276.1; -.
 DR HSSP: P02699; 1F88.
 DR ZFIN: ZDB-GENE-980526-393; npry1A.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 DR Receptor.
 KW RECEPTOR.
 SQ SEQUENCE 377 AA; 42901 MW; 60E6ZAD9C7BFED50 CRC64;

Query Match 33.6%; Score 617.5; DB 13; Length 377;
 Best Local Similarity 37.1%; Pred. No. 1,7e-44;
 Matches 124; Conservative 66; Mismatches 133; Indels 11; Gaps 4;

QY 20 NKTATENNFAATRNSEDPVWDYKSSVDLQYFLIGLYTFVSLIGFMGNLITMALMK 79
 Db NSTLTTHQNSNSFLLDVPCW--QSSMTLT--LVLCYCLVILIGLNLITLITIMHQ 70
 QY 80 NQKTTVNFILGNLAFSDILVLEFCSPFTLTSLVLDQMMEGKVNCHIMPLOCVSLVST 139
 Db 71 RDPNVTSLILANLSVDILVSCFLPFTVYTLMDHMFALLCRMLPFCQCVSVTSV 130
 QY 140 LILISIAIVRHMKHPISNNLTHNGYFLIATVTLGFAICSPLPVPHSLVELOETFGS 199
 Db 131 LSLVLALIERQQLIHESGKMPKVPQAYIAVLTWMLACVTSLEPFAFHLLTSEPSLFP 190
 QY 200 ALLSSRYLCVESWPSDSYRIAFITSLVQYTLPLVCLTVSHTSVCTLRKRNMMDKM- 258
 Db 191 APLSQLOVCEFWPSQDHKLAITYTSLIFQCCPLLMLCYLRIFLQLRREMLEKOC 250
 QY 259 ----RDNKYSSRSRSRYFRLTILVFAVSMPLHLFHVVTDENMLISNRHKLVCYCI 314
 Db 251 SRNEDERHRRVMSKRINVMATLVAAFAVCWMLPLNAFNVAADCQEVLEPVCNNLLFSL 310
 QY 315 CHLLGMSCCLNPILYGLFNLNGIKADLVSLI-HC 347
 Db 311 CHLLAMSTCVNPIYGLFNLNFKRDVAAVYLHC 344

RESULT 7
 OBOGM3 PRELIMINARY; PRT; 377 AA.
 AC OBOGM3;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Neuropeptide y receptor 4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lundell I., Boswell T., Larhammar D.;
 RT "Chicken Neuropeptide y Family Receptor y4; a Receptor with Equal
 RT Affinity for Pancreatic Polypeptide, Neuropeptide y and Peptide YY.";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF410853; AAL84161.1; -.
 DR Receptor.
 KW SEQUENCE 377 AA; 42972 MW; C9EC6C00DBFD19E CRC64;

Query Match 31.5%; Score 578; DB 13; Length 377;
 Best Local Similarity 34.6%; Pred. No. 3.9e-41;
 Matches 119; Conservative 78; Mismatches 129; Indels 18; Gaps 8;

QY 20 NKTATE-----NNTAATRNSEDPV-WDDYKSSVDLQYFLIGLYTFVSLIGFMGNLI 72
 Db 2 NKTAAVHAPFELNNKNNLSNRSPSHLSNCCRWVTLDTLATSLSLETVLGIVGNCL 61
 QY 73 LMAIMKRNQKTTVNFILGNLAFSDILVLEFCSPFTLTSLVLDQMMEGKVNCHIMPLOEC 132
 Db 62 IAVIARQEKTNVTNIIISLISIDLEFCVLCLEPFTVYTWMDWIGEVCKMTSTQC 121
 QY 133 VSVLSTLILISIAIVRHMKHPISNNLTHNGYFLIATVTLGFAICSPLPVPHSLV- 191
 Db 122 TSVVSTLSLVLALIERQQLINPTGMRPSISQAYLIGVYWT--ACLSMLPPLTISIL 179
 QY 192 --ELQETFGSALLSSRY--LCVESWPSDSYRIAFITSLVQYTLPLVCLTVSHTSVCI 246
 Db 180 SNDLYEQL-SHINNFYSYDKAICIDSWPSEQHRLIYTTLLTLLQYICIPLEFIICLYRIYL 238
 QY 247 RLKRRNNMMDKMRDNKRSSRSRSRYFRLTILVFAVSMPLHLFHVVTDENMLISNR 306
 Db 239 RLQRKDMFEK-SEYSNRNAVQLRINILASMAFAVCWMLPLHVFPTVDMYKIIISPC 297
 QY 307 HFKLVYCIHLLGMSCCLNPILYGLFNLNGIKADLVSLI-HCLH 349
 Db 298 HNLIFSLCHLVMASTCVNPIYGLFNLNFKRKVKSLISQH 341

RESULT 8
 OQYHX1 PRELIMINARY; PRT; 374 AA.
 AC OQYHX1;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Neuropeptide y/peptide yy receptor Yb.
 GN NPYRB
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99017378; PubMed-9802392;
 RA Arvidsson A.K., Waith A., Jonsson-Rylander A.C., Larhammar D.;
 RT "Cloning of a neuropeptide y/peptide yy receptor from the Atlantic
 RT cod: the Yb receptor";
 RL Regul. Pept. 75:39-43(1998).
 DR EMBL: AF073925; AAD02833.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE 374 AA; 42260 MW; D2A9C9516C4998E2 CRC64;

Query Match 30.2%; Score 554.5; DB 13; Length 374;
 Best Local Similarity 35.2%; Pred. No. 3.7e-39;
 Matches 108; Conservative 67; Mismatches 113; Indels 19; Gaps 5;

QY 53 FLIGLYTFVSLIGFMGNLILMALMKRNQKTTVNFILGNLAFSDILVLEFCSPFTLTSV 112
 Db 39 FLILVSTMTAVGIVGNSCLVFAVIAKQEMHNVTNIFIANLSCSDILMFCFLPVTLIYT 98
 QY 113 LLDQMMEGKVNCHIMPLOCVSVLSTLISIAIVRHMKHPISNNLTHNGYFLIAT 172
 Db 99 LMDRWILGEALCKLPVQCISVTSVLSVLAMERYQLIHPTGKPKVAGSYMAVGT 158
 QY 173 VWT-----LGFAICSPLPVPHSLVELOETFGSALLSSRYLCVESWPSDSYRIAFIT 223
 Db 159 IMVYACISVPLSFYLDLP----LQNSLSEPPG---QDHMLCTESWFTNSRLAYTT 211
 QY 224 SLLVLYIPLVCLTVSHTSVCTLRKRNMMMDKMRDNK--YSSRSRSRYFRLTILV 261

Dd	212	SLLVQYFELPLGLIACLYSLIFLRRLRRKDMVERAROSSRDNRANGSRRIINMLCSYAL	271
Oy	282	FASVMMPHLFFVVVDNDNLISNHRFKLVYCICHLGMSGCCNPILTYGFINNIGAKDL	341
Dd	272	FAVCGLRPLNFITFTVEDMHELMASCOHNLITEFVCHLVMASIVCNPVYYGFLNSFGOKL	331
Oy	342	-VSLIHC 347 : : : :	
Dd	332	KATLSHC 338	
RESULT 9			
ID	057463	PRELIMINARY:	PRT: 375 AA.
AC	057463:		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	Neuropeptide Y /peptide yy receptor Yb.		
GN	NPYRYB.		
OS	Brachydanio rerio (Zebrafish) (zebra danio).		
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OX	Cyprinidae; Danio.		
NCBI_TaxID=7955;	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R.,		
RA	Larhammar D.;		
RT	"Cloning and characterization of a novel neuropeptide Y (NPY) receptor		
RT	subtype in the zebrafish."		
RL	DNA Cell Biol. 0:0-0(1997)."		
DR	EMBL; AF030245; AAB94616.1; "		
DR	ZFIN; ZDB-GENE-980526-208; npyryb.		
DR	InterPro: IPRO000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRRHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.		
SW	Receptor.		
SC	SEQUENCE 375 AA; 42116 MW; 4BDC9551131A14D1 CRC64;		
Query Match 29.4%; Score 539; DB 13; Length 375;			
Best Local Similarity 33.8%; Pred. No. 7.7e-38;			
Matches 101; Conservative 68; Mismatches 122; Indels 8; Gaps 3;			
Oy	53	FLIGLTYSVLGGNGNLIILMALKKRKQKTTFNFLIGNLAFSDILVYLFCSPETLSIV	112
Dd	27	FLIVATYSTPLAVGLAGVINCCLVVIITROKEMRWVTNIFINLISCDIQLCVLCVLPVITYT	86
Oy	113	LDDOMFGVKMHIMPFLQCVSVLSTLLISIAIVRYMKIKPTISNNLTANHGVELINT	172
Dd	87	LMDRNIIIGLCAICKYTPFYQCKMSVTVSIPTSMVALDERHOLIHPGMKRVYAHSLAAV	146
Oy	173	VWTLGFAICSPLPVPHSLV-----ELQETEGSALLSRYLCVESMPDSYRIAFTISLL	227
Dd	147	IWLICEFSISLPESLNITNSPFNHLISLPFN--FSDHFICIEQMPSSEGRNLTYTTILL	204
Oy	228	VYTIPLVLCVTSYSHRSVCRLKRKNMMDKMDKNKYRSSR-SRSFYRLTILILYFAVSM	286
Dd	205	CCYCTPLAILVLCYCRIFRLTSRRDKVERAAGRGQRKAKGSKRNVAMLASTVAAPALCW	264
Oy	287	MPLHLFHVVTDPNDNLISNRHFKLVYCICHLGMSGCCNPILTYGFLNNGICADLVSLI	345
Dd	265	LPLNVEFTLFDMNHHAIPVCGHDAIFSACHLTAMAASTCVNPVIYTGFLNNFPQELKSLL	323
RESULT 10			
ID	08UVW7	PRELIMINARY:	PRT: 365 AA.
AC	08UVW7:		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		

[illegible]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRED NORWEGIAN LANDRACE;
 RX MEDLINE=20187975; PubMed=10720571;
 RA Walith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,
 RA Andersson L., Lundin L.-G., Larhammar D.;
 RT "Evolution of the neuropeptide Y receptor family: gene and chromosome
 RT duplications deduced from the cloning and mapping of the five receptor
 RT subtype genes in the pig."
 RL Genome Res. 10:302-310(2000).
 DR EMBL: AB021678; BAA36218.1; -
 DR EMBL: AF227955; AAF62507.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
 KW Neuropeptide; Receptor.
 SO SEQUENCE 375 AA; 42346 MW; 5992F075904DB1A0 CRC64;

Query Match 28.2%; Score 518.5; DB 6; Length 375;
 Best Local Similarity 31.2%; Pred. No. 4.2e-36;
 Matches 102; Conservative 73; Mismatches 135; Indels 17; Gaps 5;

QY 28 NTATRNDSDFVMDYKSSVDLDYFLGLTYFVSLGFMGNLLILMALMKRNQKTVN 87
 Db 19 NRSKAKGIPYFSDHCQDSIDPM-VFVYTSISIEYVGLNCLICVTTIKOKKANVTN 77
 QY 88 FLIGNLAFSDLLVLFCSPTLTSLVDQMMGKVMCHIMPLOCVSLVSTLLISAI 147
 Db 78 LLIANLAFSDFLMCLICOPLAITYINDYVWGEVLCKISAFICQMSVTSILSLVAL 137
 QY 148 VRYMIKHPIISNNLTANHGYFLIATWTLGFAICSPL-----PVRSLVELOETFGSA 200
 Db 138 ERHOLLIPMGKPSVSQAYLGIIVIMLACFLSLPLFANSILONVFK---NHSKAVE 193
 QY 201 LLSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLVTSHTSVICIRKRRNMMDK--M 258
 Db 194 FLAKVVCESWPLRHHRIYTTFLLLFQYCIPLAVICVRYQIRKRGVFNHGAY 253
 QY 259 RDNKRSSRSRSVFYRLTILVFAVSMPLHLFHVYTDFNDLISNRHFLVYCIQHL 318
 Db 254 SSRAMQKRIINGI---LAAMVVAFAVLMPLHVFNSLEDWYHEALPICHGLIFLYCHLL 310
 QY 319 GMSCCCLNPLLYGFLNGIKADVSLI 345
 Db 311 AMASTCVNPFLYGLTNTNFKREKVALV 337

RESULT 12
 ID 073734 PRELIMINARY; PRT; 373 AA.
 AC 073734;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Neuropeptide Y/peptide Y receptor Yc.
 GN NPYRYC OR NPYRYC.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=9955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98068842; PubMed=9407007;
 RA Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
 RA Larhammar D.;
 RT "Cloning and characterization of a novel neuropeptide Y receptor
 RT subtype in the zebrafish."
 RL DNA Cell Biol. 16:1357-1363(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98096393; PubMed=9434780;

RA Ringvall M., Berglund M.M., Larhammar D.;
 RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
 RT subtype in the zebrafish."
 RL Biochem. Biophys. Res. Commun. 241:749-755(1997).
 DR EMBL: AF037401; AAC41277.1; -
 DR ZFIN: ZDB-GENE-990415-175; npyryc.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SO SEQUENCE 373 AA; 41673 MW; 217DA7F51A940CFD CRC64;

Query Match 28.1%; Score 515.5; DB 13; Length 373;
 Best Local Similarity 33.2%; Pred. No. 7.5e-36;
 Matches 100; Conservative 72; Mismatches 120; Indels 9; Gaps 4;

QY 54 LIGLTYFSLGFMGNLLILMALMKRNQKTVNFLIGNLAFSDLLVLFCSPTLTSLV 113
 Db 33 LIVASTVIAVGLVGNCLVFLISROKEMRVNILLANLSCSDILMCVCLPVTVIYTL 92
 QY 114 LDOMMFGKVMCHIMPLOCVSLVSTLLISAIYRYMIKHPIISNNLTANHGYFLATV 173
 Db 93 MDRNILEGTLCKVLPYQCKSVTVSIFSLVLIALERHOLLIPMGWTPAAGHSTLAAVT 152
 QY 174 WTLGFAICSPLPVFSLVELOETFGSALL-----SRYLCVESWPSDSYRIAFITSLV 228
 Db 153 MWVACFISLPLRSLNILL--NAPQNTSLPRNPSDHYICHELMPSENRRLATYTSLLF 210
 QY 229 QYLLPLVCLVSHRSVCIRKRRNMMDKRNKRSR--SRSVYRLTILVFAVSM 287
 Db 211 QYCLPLILILCYRLFRILRRRKDWEOATEARQARCAQRVNAMLVIVAFACWL 270
 QY 288 PLHLFHVYTDFNDLISNRHFLVYCIQHLGMSCCCLNPLLYGFLNGIKADL-VSLIH 346
 Db 271 PLVNFILPDIWYHQAIPACQHDVIFSACHILAMASTCVNPVYGLTNTNFKELKATL 330
 QY 347 C 347
 Db 331 C 331

RESULT 13
 ID 0922D4 PRELIMINARY; PRT; 372 AA.
 AC 0922D4;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Pancreatic polypeptide receptor Y4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hysticognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99017377; PubMed=9802391;
 RA Eriksson H., Berglund M.M., Holmberg S.K., Kahl U., Gehlert D.R.,
 RA Larhammar D.;
 RT "The cloned guinea pig pancreatic polypeptide receptor Y4 resembles
 RT more the human Y4 than does the rat Y4."
 RL Regul. Pept. 75:29-37(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sharma P.S., Holmberg S.K., Eriksson H., Beck-Stickinger A.G.,
 RA Grundemar L., Larhammar D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF072822; AAD13144.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.

DR	PROSITE, PSS0262; G-PROTEIN_RECER_FL_2; 1.
KM	Sequence
SO	SEQUENCE 372 AA; 41774 MW; 5B6CF8FB213374 CRC64;
	Query Match 27.9%; Score 512; DB 11; Length 372;
	Best Local Similarity 31.1%; Pred. No. 1.5e-35;
	Matches 103; Conservative 73; Mismatches 139; Indels 16; Gaps
QY	22 TLATENNTAATRNSDPFYMDYDKSSVDDLYOFLGLTFTVSLFPMGNLLTALMKRN 81
DB	13 TYPQENSSKQRIILFN-FSDHCQSDSDLMGEITVTSYGIEIYGVGLNCLICMLNQKE 71
QY	82 QKTAVNELICLAFSDILVYLFCSPFLTSLYLDQMGKVMCHIMEFLDQCVSLVSTLI 1411
DB	72 KANTSLTILALAFSDIFMLCLICQPLTIVTYITIMDYTFEGVELCKMAFIDCMSTVYILS 1311
QY	142 LISAIYRHHKIPDISNNLTANNGEYLATVWFLGFAISPL-----PVFSLVELQ 134
DB	132 LVLALEHHQILINPTGMRKSPVDAIYIGIYVILACVLSIPFLANSILENVPR----N 187
QY	195 ETFFSALLSSRYLQVESWPSDYRIAFETISLLVQYLPLVCLTFSVTCIRLRNNM 254
DB	188 HSKALAFLEDRVACKESPLGHHNVVTTPELLFQYICPLAFILYVCLRLSMRLRGGRV 247
QY	255 MDKMRNDKYRSSRSRSVFYRLTLLVPAVSWMDLH-FHWVTDENDNLISNRHFKLYCI 3144
DB	248 LCK-----SSRAQGMKRIINGVLVAVAGFAFVLMPLRLHVFNSLEDMHNAIPVCHGNLIFLV 3030
QY	315 CHLGMMSCCLNPLTGLFNLNGIADLVSLI 345
DB	304 CHLLAMASTCVNPETVGLTNFNRKRYKALV 334
RESULT 14	
Q9ERCO	PRELIMINARY; PRT; 381 AA.
AC	Q9ERCO; 01-MAR-2001 (TREMBlrel, 16, Created)
DT	01-MAR-2001 (TREMBlrel, 16, Last sequence update)
DT	01-JUN-2002 (TREMBlrel, 21, Last annotation update)
DE	Neuropeptide Y/peptide yy-Y2 receptor.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
CC	Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_Taxid=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Wistar; TISSUE=SMALL INTESTINE;
RA	Voisin T., Goumain M., Laburthe M.;
RT	"Cloning of a cDNA encoding a rat type 2 neuropeptide Y/peptide YY
RT	receptor expressed in intestinal epithelial crypt cells."
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL, AY004257; AAF89094.1; -
DR	InterPro: IPR000276; GPCR_Rhodopsin.
DR	InterPro: IPR001220; Lectin_1egb.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS: PR00237; GPCRHDOPSN.
DR	PRINTS: PR01570; NPFRECEPTOR.
DR	PROSITE: PS00237; G-PROTEIN_RECER_FL_1; UNKNOWN_1.
DR	PROSITE: PSS0262; G-PROTEIN_RECER_FL_2; 1.
DR	PROSITE: PSS0307; LECTIN_LEGUEM_BETA; UNKNOWN_1.
KW	Receptor.
SO	SEQUENCE 381 AA; 42510 MW; 659327904B288BC7 CRC64;
	Query Match 27.4%; Score 503; DB 11; Length 381;
	Best Local Similarity 32.2%; Pred. No. 8.8e-35;
	Matches 98; Conservative 75; Mismatches 117; Indels 14; Gaps
QY	49 DLQYFLGLTFTVSLDFPMGNLLTALMKRNKQNTAVNELICLAFSDILVYLFCSPFT 108
DB	48 EVQYVLLATCSITLLGVGNSLVIHYIKFSKRYTYNPFANLAVADLVNTLCIPIPT 107
QY	109 LTVSLDQMGKVMCHIMEFLDQCVSLVSTLILISAIYRHHKIPDISNNLTANNGYF 168

QY	DB	Query Match	Best Local Similarity	Matches	Score	DB 5	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414
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Mon Nov 25 08:49:29 2002

us-09-771-956-6.rspt

Page 8

QY 303 ISNRFFKLYVCITHLGMSCCNLILYFFLNNGIKADVLSIT 345
::: | |||: || | |||: ||: : : | :
Db 343 VT-OSMLVYATICHMIGSSACSNPLDYLWLNDFRRFFQELL 384

Search completed: November 22, 2002, 13:10:26
Job time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:05:43 ; Search time 14 Seconds

(without alignments)
1036.908 million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836

Sequence: 1 MSFYSKODYNMDELDEYYN.....GFLNGIKADLVSLHCLHM 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1668.5	90.9	455	1	NPYR_HUMAN
2	1581.5	86.1	446	1	NPYR_CANFA
3	1536	83.7	456	1	NPYR_RAT
4	1534.5	83.6	446	1	NPYR_PIG
5	1514.5	82.5	466	1	NPYR_MOUSE
6	650	38.2	382	1	NPYR_CANFA
7	650	35.4	383	1	NPYR_PIG
8	644	35.1	384	1	NPYR_HUMAN
9	640.5	34.9	383	1	NPYR_CANFA
10	637	34.7	366	1	NPYR_XENLA
11	633.5	34.5	382	1	NPYR_MOUSE
12	633.5	31.4	371	1	NPYR_RABIT
13	576.5	31.4	371	1	NPYR_MOUSE
14	552.5	30.1	371	1	NPYR_MOUSE
15	525	28.6	385	1	NPYR_CHICK
16	515.5	28.1	375	1	NPYR_MOUSE
17	515	27.5	375	1	NPYR_HUMAN
18	505.5	27.5	375	1	NPYR_RAT
19	505	27.5	381	1	NPYR_CANFA
20	504	27.5	381	1	NPYR_HUMAN
21	503	27.4	385	1	NPYR_MOUSE
22	501	27.3	384	1	NPYR_BOVIN
23	497	27.1	381	1	NPYR_MACMU
24	496	27.0	382	1	NPYR_PIG
25	464	25.3	370	1	GP10_HUMAN
26	453.5	24.7	370	1	GP10_RAT
27	421.5	23.0	449	1	NPYR_MOUSE
28	397.5	21.7	455	1	NPYR_MOUSE
29	380.5	20.7	432	1	NPYR_MOUSE
30	378.5	20.6	423	1	NPYR_MOUSE
31	377.5	20.6	417	1	NPYR_MOUSE
32	375.5	20.4	453	1	NPYR_MOUSE
33	374	20.4	522	1	NPYR_MOUSE

ALIGNMENTS

RESULT 1	STANDARD	PRT	AA
NPYR_HUMAN			
AC	015761; Q92916;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor) (NPY5)		
GN	NPYR OR NPYR5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Hippocampus;		
RX	MEDLINE=96317589; PubMed=8700207;		
RA	Gerald C., Walker M.W., Ciscione L., Gustafson E.L., Laz T.M., Batzli-Hartmann C., Smith K.E., Vaysses P., Durkin M.M., Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G., Taber R.I., Branchek T.A., Weinschenk R.L.;		
RA	"A receptor subtype involved in neuropeptide-Y-induced food intake,"		
RT	Nature 382:168-171(1996).		
RL	[2]		
RP	SEQUENCE OF 11-455 FROM N.A.		
RX	MEDLINE=96421636; PubMed=8824284;		
RA	Hu Y., Bloemquist B.T., Cornfield L.J., Decarr L.B., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L., Sedlowski Y., Schaefer J., Velazquez N., McCabe M.L.;		
RA	"Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior,"		
RT	J. Biol. Chem. 271:26315-26319(1996).		
RL	[3]		
RP	SEQUENCE OF 11-455 FROM N.A.		
RX	MEDLINE=97312666; PubMed=9169127;		
RA	Herzog H., Darby K., Ball H., Hort Y., Beck-Sickinger A., Shine J.;		
RT	"Overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation,"		
RL	Genomics 41:315-319(1997).		
CC	-1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: BRAIN; HYPOTHALAMUS.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		

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CC -----
DR EMBL: U56079; AAC50623.1; -
DR EMBL: U66275; AAC50741.1; -
DR EMBL: U94320; AAC51295.1; -
DR Genbank: HGNC:7958; NPY5R.
DR MIM: 602001; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 72 1 (POTENTIAL).
FT DOMAIN 73 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 147 3 (POTENTIAL).
FT DOMAIN 148 167 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 168 188 4 (POTENTIAL).
FT DOMAIN 189 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 242 5 (POTENTIAL).
FT DOMAIN 243 321 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 321 401 6 (POTENTIAL).
FT DOMAIN 402 414 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 415 438 7 (POTENTIAL).
FT DOMAIN 439 455 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 124 208 BY SIMILARITY.
FT LIPID 452 452 PALMITATE (POTENTIAL).
SQ SEQUENCE 455 AA; 51990 MW; 95F2747E5FB8F7 CRC64;

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Query Match          90.9%; Score 1668.5; DB 1; Length 455;
Best Local Similarity 73.2%; Pred. No. 6.1e-96;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

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QY 1 MSFYSKQDYNNDELDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLDQYFLIGLYTF 60
DB 1 MSFYSKQDYNNDELDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLDQYFLIGLYTF 60
QY 61 VSLIGFMGNLLILALMKRRKQKTVNFLIGNAFSDILVVFCSPTFLTSVLDQWMEG 120
DB 61 VSLIGFMGNLLILALMKRRKQKTVNFLIGNAFSDILVVFCSPTFLTSVLDQWMEG 120
QY 121 KVMCHIMFLOCVSVLSTLISIAIVRYHMKHPISNNLTANGYFLIATVMTLGPAT 180
DB 121 KVMCHIMFLOCVSVLSTLISIAIVRYHMKHPISNNLTANGYFLIATVMTLGPAT 180
QY 121 KVMCHIMFLOCVSVLSTLISIAIVRYHMKHPISNNLTANGYFLIATVMTLGPAT 180
DB 121 KVMCHIMFLOCVSVLSTLISIAIVRYHMKHPISNNLTANGYFLIATVMTLGPAT 180
QY 181 CSPLPVEHSLVELOETFGSALLISRYLCVESWPSDYRIAFITISLLVOYTLPLVCLTVS 240
DB 181 CSPLPVEHSLVELOETFGSALLISRYLCVESWPSDYRIAFITISLLVOYTLPLVCLTVS 240
QY 241 HTSYC-----ILKRRNNMDK----- 257
DB 241 HTSYC-----ILKRRNNMDK----- 257
QY 241 HTSYC-----ILKRRNNMDK----- 257
DB 241 HTSYC-----ILKRRNNMDK----- 257
QY 258 -----MRDNKRR----- 264
DB 258 -----MRDNKRR----- 264
QY 301 KKTACVLPAPERPSQENISRIILPENFGSVRSQSSSKFICGVPCTCFIKRENSDVHEL 360
DB 301 KKTACVLPAPERPSQENISRIILPENFGSVRSQSSSKFICGVPCTCFIKRENSDVHEL 360
QY 361 RVKRSVTEIKRRSRVSVEFYRTILILVFASWMPDLHLFHVVDDEFNDNLISNRHFKLVYCIC 420
DB 361 RVKRSVTEIKRRSRVSVEFYRTILILVFASWMPDLHLFHVVDDEFNDNLISNRHFKLVYCIC 420
QY 421 HLLGMMSGCLNPIIXGLFNNGIKADVSLHICLHM 455
DB 421 HLLGMMSGCLNPIIXGLFNNGIKADVSLHICLHM 455

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RESULT 2
ID NYSR_CANFA STANDARD: PRT: 446 AA.

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AC 062729;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5
DE receptor) (NPY5).
GN NPY5R OR NPY5.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99017379; Pubmed=9802393;
RA Borowsky B., Walker M.W., Bard J., Weinschenk R.L., Laz T.M.,
RA Vaysses P., Branchek T.A., Gerald C.
RT "Molecular biology and pharmacology of multiple NPY Y5 receptor
RT species homologs."
RL Regul. Pept. 75:45-53(1998).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
CC BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF049328; AAC17838.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
  Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 62 1 (POTENTIAL).
FT DOMAIN 63 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 94 2 (POTENTIAL).
FT DOMAIN 96 115 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 116 137 3 (POTENTIAL).
FT DOMAIN 138 157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 158 178 4 (POTENTIAL).
FT DOMAIN 179 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 232 5 (POTENTIAL).
FT DOMAIN 233 311 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 369 391 6 (POTENTIAL).
FT DOMAIN 392 404 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 405 428 7 (POTENTIAL).
FT DOMAIN 429 446 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 114 198 BY SIMILARITY.
FT LIPID 442 442 PALMITATE (POTENTIAL).
SQ SEQUENCE 446 AA; 51012 MW; 5CAB8D2CF5D254A CRC64;

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Query Match          86.1%; Score 1581.5; DB 1; Length 446;
Best Local Similarity 71.7%; Pred. No. 1.3e-99;
Matches 319; Conservative 7; Mismatches 14; Indels 105; Gaps 3;

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QY 11 MDLEDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70
DB 1 MDLEDEYYNKTATENTNTAATRNSDFPVMDYKSSVDLDQYFLIGLYTFVSLGFMGNL 70
QY 71 LILALMKRRKQKTVNFLIGNAFSDILVVFCSPTFLTSVLDQWMEGKVMCHIMFPL 130
DB 71 LILALMKRRKQKTVNFLIGNAFSDILVVFCSPTFLTSVLDQWMEGKVMCHIMFPL 130

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Db 61 LILMALRRKRNOKTMVNFIGNLAFSDILVLFCSPTLTSLVDLQMMFGKVMCHIMPEL 120
Oy 131 QCVSVLSTLILISIAIVRYHMIRKIPISNNLTANHGFIATVWTGFAICSPLPVESH 190
Db 121 QCVSVLSTLILISIAIVRYHMIRKIPISNNLTANHGFIATVWTGFAICSPLPVESH 180
Oy 191 VELOEFGSALLSRVYCVSWPDSYRIAFITISLLVOTILPLVCLTVSHTSVC----- 245
Db 181 VELOEFGSALLSRVYCVSWPDSYRIAFITISLLVOTILPLVCLTVSHTSVC----- 240
Oy 246 -----IRLKR----- 251
Db 241 GLSKENKLEENEMINTLOPFKSSQPVKLVSSHKMSYSFIRKRRRYSKKTACVLPAP 300
Oy 252 -----NNMDKMRDNK---YRS 265
Db 301 APPQENHSHMLPENFGSVRSQHSKSFIPGVPTCFECPKPEKSDVHDMKVRNSIMRIK 360
Oy 266 SRSSVYFRTITLILVAVSWMPLEFHYVTDPNDLISNRHFLVYCICHLGMSGCL 325
Db 361 KRSSVYFRTITLILVAVSWMPLEFHYVTDPNDLISNRHFLVYCICHLGMSGCL 420
Oy 326 NPILYGLNNGIKADVLVSLJHCLM 350
Db 421 NPILYGLNNGIKADVLVSLJHCLM 445

RESULT 3
NY5R_RAT STANDARD; PRT: 456 AA.
ID NY5R_RAT
AC 063634; P70586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).
GN NPY5R OR NPYR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=96317589; PubMed=8700207; Gerald C., Walker M.W., Criscione L., Gustafson E.L., Batzli-Hartmann C., Smith K.E., Vayese P., Durkin M.M., Laz T.M., Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hobbauer K.G., Taber R.I., Branchek T.A., Weisshank R.L.; "A receptor subtype involved in neuropeptide-Y-induced food intake." Nature 382:168-171(1996).
RL Nature 382:168-171(1996).
RN [2]
RP SEQUENCE OF 12-456 FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98332165; PubMed=9669502; Parker E.M., Babil C.K., Balasubramaniam A., Butrier R.E., Guzzi M., Hamud F., Mukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L., Mullins D.E., Salisbury B.G.; "GR231118 (1229U91) and other analogues of the C-terminus of neuropeptide Y are potent neuropeptide Y Y1 receptor antagonists and neuropeptide Y Y4 receptor agonists." Eur. J. Pharmacol. 349:97-105(1998).
RN [3]
RP SEQUENCE OF 12-456 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=96421636; PubMed=8824284; Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L., Sadowski Y., Schaefer J., Velazquez N., McCabe M.L.; "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior." J. Biol. Chem. 271:26315-26319(1996).
RL J. Biol. Chem. 271:26315-26319(1996).
-i- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
```

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CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
CC BE INVOLVED IN FEEDING DISORDERS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN; HYPOTHALAMUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U56078; AAC52677.1; -.
DR EMBL: AF044264; AAC15670.1; -.
DR EMBL: U66274; AAC52845.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 50
FT TRANSMEM 52 73
FT DOMAIN 74 85
FT TRANSMEM 86 106
FT DOMAIN 107 126
FT TRANSMEM 127 148
FT DOMAIN 149 168
FT TRANSMEM 169 189
FT DOMAIN 190 221
FT TRANSMEM 222 243
FT DOMAIN 244 322
FT TRANSMEM 379 401
FT DOMAIN 402 414
FT TRANSMEM 415 438
FT DOMAIN 439 456
FT DISULFID 125 209
FT LIPID 452 452
FT CARBOHYD 21 21
FT CARBOHYD 28 28
SQ SEQUENCE 456 AA; 51715 MW; 5157ABE341BA707E CRC64;

Query Match 83.7%; Score 1536; DB 1; Length 456;
Best Local Similarity 67.9%; Pred. No. 8,2e-88;
Matches 304; Conservative 21; Mismatches 19; Indels 104; Gaps 3;

Oy 7 QDYNMDELDEYNNKTATENTNNTAATNSDFPVWDVYKSSVDDLOQYFLIGLYTFVSLGF 66
Db 8 QDSMERKLEHNRKTVTENNTAARNNAFPAWEDRGSDVDDLOQYFLIGLYTFVSLGF 67
Oy 67 MGNLLILMALMKRRNOKTTVNPLIGNLAFSDILVLFCSPTLTSLVDLQMMFGKVMCH 126
Db 68 MGNLLILMALMKRRNOKTTVNPLIGNLAFSDILVLFCSPTLTSLVDLQMMFGKVMCH 127
Oy 127 MPFLOQSVSVLSTLILISIAIVRYHMIRKIPISNNLTANHGFIATVWTGFAICSPLP 186
Db 128 MPFLOQSVSVLSTLILISIAIVRYHMIRKIPISNNLTANHGFIATVWTGFAICSPLP 187
Oy 187 FHSVLELOEFGSALLSRVYCVSWPDSYRIAFITISLLVOTILPLVCLTVSHTSVC- 245
Db 188 FHSVLELOEFGSALLSRVYCVSWPDSYRIAFITISLLVOTILPLVCLTVSHTSVC 247
Oy 246 ---IRLKRNNMMDK-----MRDNKYRS----- 266
Db 248 SISCSGLSKENKLEENEMINTLOPSKRSRNOAKTSTQKMSYSFIRKRRRYSKKTACV 307
Oy 267 ----- 266
Db 308 LPAPAGPSGCKHLAVPENPASVRSQSPSKVLPGVPTCFECPKPESSDAHEKVRKRSIT 367
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QY 267 ----RSRSVFRRLTLLILVEAVSWMPDLHVFVTDNDNLISNRHFKLVYCICHLGMS 322
 DB 368 RIKRSRSVFRRLTLLILVEAVSWMPDLHVFVTDNDNLISNRHFKLVYCICHLGMS 427
 QY 323 CCLNPILYGLFNGIKADLVSLHICLHM 350
 DB 428 CCLNPILYGLFNGIKADLVSLHICLHM 455

RESULT 4
 NY5R_PIG STANDARD; PRT; 446 AA.
 AC 097969;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor)
 GN NPY5R OR NPYR5.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wraith A., Torsten A., Chardon P., Harbitz I., Chowdhary B.P., Anderson L., Larhammar D.;
 RT Porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and comparative analysis";
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMD; TISSUE=Kidney;
 RA Ito Y., Minezawa M.;
 RT "Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO TACHYKININS RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: AF106083; AAD13778.1;
 DR EMBL: AB019185; BA34055.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 39
 FT TRANSMEM 41 62
 FT DOMAIN 63 74
 FT TRANSMEM 75 95
 FT DOMAIN 96 115
 FT TRANSMEM 116 137
 FT DOMAIN 138 157
 FT TRANSMEM 158 178
 FT DOMAIN 179 210
 FT TRANSMEM 211 232
 FT DOMAIN 233 311

FT TRANSMEM 369 391 6 (POTENTIAL).
 FT DOMAIN 392 404 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 405 428 7 (POTENTIAL).
 FT DOMAIN 429 446 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 114 198 BY SIMILARITY.
 FT LIPID 442 442 PALMITATE (POTENTIAL).
 SQ SEQUENCE 446 AA; 50474 MW; B7F616C2394C6CA0 CRC64;

Query Match 83.6%; Score 1534.5; DB 1; Length 446;
 Best Local Similarity 68.8%; Pred. No. 9.9e-88;
 Matches 306; Conservative 17; Mismatches 17; Indels 105; Gaps 3;

QY 11 MDLEDEYVYKNTLATENNATATNSDPVWDYKSSVDLDQYFLIGHYTEYSLGFGMNL 70
 DB 1 MGSLEIPYKNTLATSENNVATRNSGFVWEDYKGSVDLDQYFLIGHYTEYSLGFGMNL 60
 QY 71 LILMAKKRRNQKTYVNFIGNLAFSDILVVLFCSPPTLTSVLLDQWMEGKVMCHIMPTL 130
 DB 61 LILMAVRRKRNQKTYVNFIGNLAFSDILVVLFCSPPTLTSVLLDQWMEGKVMCHIMPTL 120
 QY 131 QCVSVLVSTLLISIAIVRYHMKHPTISNNITANHGFLATVWTGLFATCSPLPVRHSL 190
 DB 121 QCVTVLVSTLLISIAIVRYHMKHPTISNNITANHGFLATVWTGLFATCSPLPVRHSL 180
 QY 191 VELQETFGSALLSRVYCVESWPSDSYRIAFITSLLVQYTLPLVCLTVSHTSVC----- 245
 DB 181 VELQETFGSALLSRVYCVESWPSDSYRIAFITSLLVQYTLPLVCLTVSHTSVCRTISC 240
 QY 246 -----IRLKR----- 251
 DB 241 GLSSQDSKLEENEMINLTLPKRKSGPQAKLSHPKWTYSFIRRRRRYSKTCVAPAP 300
 QY 252 -----NNMDKKRDNK-----YRS 265
 DB 301 AGPLEREGRPCKVGSWOSOPPSKKNPVCVTCPEVKEENSDVPEKVVSTIRLR 360
 QY 266 SRSRSVFRRLTLLILVEAVSWMPDLHVFVTDNDNLISNRHFKLVYCICHLGMS 325
 DB 361 KRSSRSVFRRLTLLILVEAVSWMPDLHVFVTDNDNLISNRHFKLVYCICHLGMS 420
 QY 326 NPILYGLFNGIKADLVSLHICLHM 350
 DB 421 NPILYGLFNGIKADLVSLHICLHM 455

RESULT 5
 NY5R_MOUSE STANDARD; PRT; 466 AA.
 ID 070342; O35380; Q9JMK1;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-5 receptor) (Y5 receptor)
 GN NPY5R OR NPYR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99017379; PubMed=9802393;
 RA Borowsky B., Walker M.W., Bard J., Weinschenk R.L., Laz T.M., Vayssie P., Branchek T.A., Gerald C.;
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";
 RT Regul. Pept. 75:45-53(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Brain;
 RA Chen H., Adams S., McWhinnie E., Bayne M., Gadsdill R., Zastawny R.;

"Mouse neuropeptide Y Y5 receptor characterized by repeat sequence in extracellular domain.";
RT Submitted (Sep-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-97459646; PubMed-9315606;
RA Nakamura M., Yokoyama M., Watanabe H., Matsunoto T.;
RT "Molecular cloning, organization and localization of the gene for the mouse neuropeptide Y-Y5 receptor.";
RL Biochem. Biophys. Acta 1328:83-89(1997).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.

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CC EMBL: AF049329; AAC17839.1; -
DR EMBL: AF022948; AAB81829.1; -
DR EMBL: AB001346; BAA89538.1; -
DR MGD: MGI:108082; Npy5r.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN-RECEP_FL1; FALSE_NEG.
DR PROSITE: PS50262; G-PROTEIN-RECEP_FL2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 11 60
TRANSMEM 62 83
FT DOMAIN 84 95
TRANSMEM 86 116
FT DOMAIN 117 136
TRANSMEM 137 158
FT DOMAIN 159 178
TRANSMEM 179 199
FT DOMAIN 200 231
TRANSMEM 232 253
FT DOMAIN 254 332
TRANSMEM 389 411
FT DOMAIN 412 424
TRANSMEM 425 448
FT DOMAIN 449 466
TRANSMEM 467 484
FT DISULFID 135 219
LIPID 462 462
FT CARBOHYD 10 10
CARBOHYD 17 17
FT CARBOHYD 38 38
CARBOHYD 39 39
FT CARBOHYD 195 195
CONFLICT 284 284
FT CONFLICT 284 284
SO SEQUENCE 466 AA; 52784 MW; B15F236E2D4385 CRC64;

Query Match 82.5%; Score 1514.5; DB 1; Length 466;
Best Local Similarity 65.6%; Pred. No. 1.7e-86;
Matches 305; Conservative 19; Mismatches 16; Indels 125; Gaps 5;

QY 11 MDLEDEYIKTATENTAT-----RNSDPYWDYKSSVDD 49
Db 1 MEVLEHEHFKITVTENNTAASONTASPAWEDYRGTEENTSAARNFAFPWEDYRGSVDD 60
OY 50 LQYFLGLTFFVSLGFMGNLILMALMKRKNOKTYVNFILGNLAFSDILVLFCSFETL 109
Db 61 LQYFLGLTFFVSLGFMGNLILMALMKRKNOKTYVNFILGNLAFSDILVLFCSFETL 120

QY 110 TSVLLDQWFMFGKYCHIMPLQCVSLVSLIISIAIVRYHMIKIPISNNLTANHCYFL 169
Db 121 TSVLLDQWFMFGKAMCHIMPLQCVSLVSLIISIAIVRYHMIKIPISNNLTANHCYFL 180
QY 170 IATVWTLGFAICSPLPYFHSVLVLEQEFSGALLSKRLCYESNPSDXYIAFTISLLVQ 229
Db 181 IATVWTLGFAICSPLPYFHSVLVLEQEFSGALLSKRLCYESNPSDXYIAFTISLLVQ 240
QY 230 YIIPLVCLTYSHTSVC-----IRLKRNNMMD-----KMRD----- 260
Db 241 YIIPLVCLTYSHTSVCNCSISGSLSHKENRLENDMINLTHPSKKSDDAKKPTQKMY 300
QY 261 ---NRYR----- 264
Db 301 SFIRKRRRYSKKTACVLPAPAGPSQEKHLTPENPGSVRSQSLSPSKVIPGPICFEYK 360
QY 265 -----SSRSRYVYRTILILVFAVSMPLHLFHYVTDRNDNLISN 305
Db 361 PESSDAQENRKYRSILTRIKRRRSRYVYRTILILVFAVSMPLHLFHYVTDRNDNLISN 420
QY 306 RHRKLVYCIHLLGMMSCLNPILYGFLNGIRADVSLIHCILHM 350
Db 421 RHRKLVYCIHLLGMMSCLNPILYGFLNGIRADVSLIHCILHM 465

RESULT 6
NYLR_CANFA
ID NYLR_CANFA STANDARD; PRT; 382 AA.
AC 002813;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DR Neuropeptide Y receptor type 1 (Npy1-R).
GN NPY1R.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99077380; PubMed-9802394;
RA Malmstrom R.E., Hoekfelt T., Bjorkman J.-A., Nihlen C., Bystrom M., Ekstrand A.J., Lundberg J.M.;
RT "Characterization and molecular cloning of vascular neuropeptide Y receptor subtypes in pig and dog.";
RL Regul. Pept. 75:55-70(1998)
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.

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CC EMBL: AF005778; AAC08046.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN-RECEP_FL1; 1.
DR PROSITE: PS50262; G-PROTEIN-RECEP_FL2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 38
TRANSMEM 39 61
FT DOMAIN 62 71
TRANSMEM 72 93
FT DOMAIN 94 113
EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	114	135	3	(POTENTIAL).
FT <th>DOMAIN</th> <th>136</th> <th>155</th> <th>4</th> <th>CYTOPLASMIC (POTENTIAL).</th>	DOMAIN	136	155	4	CYTOPLASMIC (POTENTIAL).
FT <th>TRANSMEM</th> <th>156</th> <th>176</th> <th>5</th> <th>EXTRACELLULAR (POTENTIAL).</th>	TRANSMEM	156	176	5	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <th>177</th> <th>209</th> <th>6</th> <th>CYTOPLASMIC (POTENTIAL).</th>	DOMAIN	177	209	6	CYTOPLASMIC (POTENTIAL).
FT <th>TRANSMEM</th> <th>210</th> <th>231</th> <th>7</th> <th>EXTRACELLULAR (POTENTIAL).</th>	TRANSMEM	210	231	7	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <th>232</th> <th>262</th> <th>8</th> <th>CYTOPLASMIC (POTENTIAL).</th>	DOMAIN	232	262	8	CYTOPLASMIC (POTENTIAL).
FT <th>TRANSMEM</th> <th>263</th> <th>285</th> <th>9</th> <th>EXTRACELLULAR (POTENTIAL).</th>	TRANSMEM	263	285	9	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <th>286</th> <th>298</th> <th>10</th> <th>CYTOPLASMIC (POTENTIAL).</th>	DOMAIN	286	298	10	CYTOPLASMIC (POTENTIAL).
FT <th>TRANSMEM</th> <th>299</th> <th>322</th> <th>11</th> <th>CYTOPLASMIC (POTENTIAL).</th>	TRANSMEM	299	322	11	CYTOPLASMIC (POTENTIAL).
FT <th>DOMAIN</th> <th>323</th> <th>382</th> <th>12</th> <th>CYTOPLASMIC (POTENTIAL).</th>	DOMAIN	323	382	12	CYTOPLASMIC (POTENTIAL).
FT <th>CARBOHYD</th> <th>2</th> <th>2</th> <th>13</th> <th>N-LINKED (GLCNAc. . .) (POTENTIAL).</th>	CARBOHYD	2	2	13	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <th>11</th> <th>11</th> <th>14</th> <th>N-LINKED (GLCNAc. . .) (POTENTIAL).</th>	CARBOHYD	11	11	14	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <th>17</th> <th>17</th> <th>15</th> <th>N-LINKED (GLCNAc. . .) (POTENTIAL).</th>	CARBOHYD	17	17	15	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <th>185</th> <th>185</th> <th>16</th> <th>N-LINKED (GLCNAc. . .) (POTENTIAL).</th>	CARBOHYD	185	185	16	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT <th>DISULFID</th> <th>112</th> <th>197</th> <th>17</th> <th>BY SIMILARITY.</th>	DISULFID	112	197	17	BY SIMILARITY.
FT <th>LIPID</th> <th>337</th> <th>337</th> <th>18</th> <th>PALMITATE (POTENTIAL).</th>	LIPID	337	337	18	PALMITATE (POTENTIAL).
FT <th>SEQUENCE</th> <th>382 AA.</th> <th>44245 MM.</th> <th>19</th> <th>95B57D20D6299803 CXC64.</th>	SEQUENCE	382 AA.	44245 MM.	19	95B57D20D6299803 CXC64.
Query Match		35.4%	Score 650;	DB 1;	Length 382;
Best Local Similarity		40.4%	Pred. No. 1.6e-33;		
Matches 127;	Conservative	64;	Mismatches 117;	Indels	6;
				Gaps	3;
OY	32	TRANSFPWDDVKSSVDDQYFLIGL-YTFVSLDFMGSLILMLMKRKNQKTYVNFLLI	90		
DB	19	SNSQSFLEFESDCHCLPLAMITFLMLAGAVITLLGVGTALIMTLIKKERNVNTILII	78		
OY	91	GNLAFSDILVLFCSPTFLSVLDDQMMGKWCIMHPELQCVSLVSTLLISIAIVRY	150		
DB	79	VNLSSDILVALMCLPFYFVYTLMDHVGEMKCLNPFVQCVSLVSTLFSVLIAVERH	138		
OY	151	HMKHPISNLTANHGYELIATVTLTGLFAICSPFLVFSHSLVELQTFGSALLSS--RYL	207		
DB	139	QLILPDCWRPNRNNHAYGVIAVITWL-AVVSLEPLIYQVLTDEPQVNTDAEKDYV	196		
OY	208	CVESPSQSYRAFLFTISLLVYLPLVCLVTSHTSVICRLKRNNMMDKMDKNKTYRSSR	267		
DB	197	CFDKPSQSHRLSYTLLMLQFGLPCLFICYPKRYIRLKRNNMMDKMDKNKTYRSSR	256		
OY	268	SRSVYRLLTILILVAVSMPLHLFHVYTDNFNDLISNHFYLCICHLGMSGCCLP	327		
DB	257	TKRIMMLSTLVAVACWMLPLTITNTYFDMNHQIATCNHNLFLCLHLTAMISTCVNP	316		
OY	328	ILYGLFNGIKADL 341			
DB	317	IFYGFLKNKFORDL 330			
RESULT 7					
NYIR_PIG					
ID	NYIR_PIG	STANDARD:	PRT:	383 AA.	
AC	002835;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Neuropeptide Y receptor type 1 (NPY1-R).				
GN	NPY1R.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Hypothalamus;				
RX	MEDLINE=99017380; PubMed=9802394;				
RA	Malmsstroem R.E., Hoekfelt T., Boerkmann J.-A., Nihlen C., Bystroem M.,				
RT	Ekstrand A.J., Lundberg J.M.;				
RT	"Characterization and molecular cloning of vascular neuropeptide Y				
RT	receptor subtypes in pig and dog.";				
RL	Regul. Pept. 75:55-70(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Wraith A., Torsten A., Chardon P., Harditz I., Chowdhary B.P.,				
RA	Andersson L., Larhammar D.;				

RT	Query Match	Score	DB 1	Length	383
RT	"Porcine NPY receptors NPY1R, NPY2R and NPY5R: Cloning, mapping and	35.4%			
RT	compatible analysis."				
RT	Submitted (NOV-1999) to the EMBL/Genbank/DBSJ databases.				
CC	- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	HIGHEST TO TRACHYKININS RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@ib-sib.ch).				
CC	-----				
DR	EMBL, AF005779; AAC26836.1; -				
DR	EMBL, AF106081; AAD13776.2; -				
DR	InterPro: IPR000276; GPCR_Rhodpsn.				
DR	Pfam: PF00001; 7tm1.1.				
DR	PRINTS: PR00237; GPCRHHODPSN.				
DR	PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.				
DR	PROSITE: PS00262; G-PROTEIN_REC_P1.2; 1.				
DR	G-protein coupled receptor; Transmembrane; Glycoprotein;				
KM	Phosphorylation; Lipoprotein; Palmitate.				
FT	DOMAIN 1 39				
FT	TRANSMEM 40 62				
FT	TRANSMEM 63 72				
FT	TRANSMEM 73 94				
FT	DOMAIN 95 114				
FT	TRANSMEM 115 136				
FT	DOMAIN 137 156				
FT	TRANSMEM 157 177				
FT	DOMAIN 178 210				
FT	TRANSMEM 211 232				
FT	DOMAIN 233 263				
FT	TRANSMEM 264 286				
FT	DOMAIN 287 299				
FT	TRANSMEM 300 323				
FT	DOMAIN 324 383				
FT	CARBOHD 2 2				
FT	CARBOHD 11 11				
FT	CARBOHD 17 17				
FT	LIPID 113 198				
FT	LIPID 338 338				
FT	CONFICT 203 203				
FT	SEQUENCE 383 AA; 44327 MW; 0058C8CA549B62CF CRC64;				
SO	SEQUENCE 383 AA; 44327 MW; 0058C8CA549B62CF CRC64;				
Query Match	35.4%; Score 650; DB 1: Length 383;				
Best Local Similarity	39.3%; Pred. No.1.6e-33;				
Matches 129; Conservative 68; Mismatches 116; Indels 15; Gaps 4;					
Y	18 YNKTLATENNTAATRNSDPEYWDYKSSVDDLYQFLIGL-YTFVSLGFGMGLLIMAL 76				
Db	15 YYN-----FSBKNSQFLAFENDDCHLPLAMIFTLALAGAVIILGVSGLALLII 65				
Y	77 MKKRKQKTTVAFLINLAFSDLVLVFCSPPFLTSVLDDQMGKVMCHMFLOCVSL 136				
Db	66 LKQKMRNVNTILLNLVSEFSDLVAMKCLPFVYVTLDDHWGEGVMKLPFVOCVSIT 125				
Y	137 VSTLLISIAIYRMIMKIPISNNLTANHGFLLTVMTLGFAICSPVPFHSVELQET 196				
Db	126 VSIPELVLAVERHOLLINPKGMRSPNNRAHYAGIAVIVL--AVASSLPFLIYQVLTPER 183				
Y	197 FGSALLSS--RYLCVESMPDSYRIATISLLIYOYLIVPLVCLTVSHTSVCIRLKRNN 253				
Db	184 FQNTVLDAFKQYVCFDKFLSDSHRLSYTLLIYLQYRGPCLCFIFTCYFKIYIRLKRNN 243				
Y	254 MADKRDNRKYSSRSRYSFYRLTLLILVFAVSMPLLPHVYTDENDNLISNRHFKLYYC 313				
Db	244 MADKRDNRKYSSRYSFYRLTLLILVFAVSMPLLPHVYTDENDNLISNRHFKLYYC 303				
Y	314 TCHLIGMSGCTINPTVYGFNLNGSTKADL 341				

Db 304 LCHLTAMISTCINPIFYGLNKNFORDL 331

RESULT 8

NY1R_HUMAN STANDARD; PRT; 384 AA.

AC P25929;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Neuropeptide Y receptor type 1 (NPY1-R).

GN NPY1R OR NPYR OR NPYL1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxId=9606;

OX

RN

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92283782; PubMed=1317848;

RA Larhammar D., Blomqvist A.G., Yee F., Jazin E.E., Yoo H., Wahlestedt C.R.;

RA "Cloning and functional expression of a human neuropeptide Y/peptide Y receptor of the Y1 type."

RT J. Biol. Chem. 267:10935-10938(1992).

RL

RN

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92335184; PubMed=1321422;

RA Herzog H., Hort Y.J., Ball H.J., Hayes G., Shine J., Selbie L.A.;

RT "Cloned human neuropeptide Y receptor couples to two different second messenger systems."

RT Proc. Natl. Acad. Sci. U.S.A. 89:5794-5798(1992).

RL

RN

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=93203272; PubMed=8095935;

RA Herzog H., Baumgartner M., Vivero C., Selbie L.A., Auer B., Shine J.;

RT "Genomic organization, localization, and allelic differences in the gene for the human neuropeptide Y Y1 receptor."

RT J. Biol. Chem. 268:6703-6707(1993).

RL

CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS NPY > (PRO-34) PYY, PYY AND (LEU-31, PRO-34) NPY > NPY (2-36) > (ILE-31, GLN-34) PP AND PYY (3-36) > PP > NPY FREE ACID.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.

CC

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CC

DR EMBL: M88461; AAA73215.1; -

DR EMBL: M84755; AAA59920.1; -

DR EMBL: L07614; -; NOT_ANNOTATED_CDS.

DR EMBL: L07615; AAA59947.1; -

DR EMBL: A26481; CAA01819.1; -

DR EMBL: A26126; CAA01787.1; -

DR PIR: A42773; A42773.

DR PIR: A46133; A46133.

DR PIR: A45490; A45490.

DR Genew; HGNC:7956; NPY1R.

DR MIM: 162641; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00023; GPCR_Rhodopsn.

DR PROSITE: PS00337; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS00337; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 39

FT TRANSMEM 40 62

FT DOMAIN 63 72

FT TRANSMEM 73 94

FT DOMAIN 95 114

FT TRANSMEM 115 136

FT DOMAIN 137 156

FT TRANSMEM 157 177

FT DOMAIN 178 210

FT TRANSMEM 211 232

FT TRANSMEM 233 263

FT TRANSMEM 264 286

FT TRANSMEM 287 299

FT TRANSMEM 300 323

FT DOMAIN 324 384

FT CARBOHYD 2

FT CARBOHYD 11 11

FT CARBOHYD 17 17

FT DISULFID 113 198

FT LIPID 338 338

FT CONFLICT 96 96

SQ SEQUENCE 384 AA; 44392 MW; 582B0DB04490316 CRC64;

Query Match 35.1%; Score 644; DB 1; Length 384;

Best Local Similarity 37.9%; Pred. No. 3.8e-33;

Matches 130; Conservative 70; Mismatches 122; Indels 21; Gaps 5;

Db 3 FYSKODYNMDELDEYNYKTLATENNTAATRNSDPWPWDYKSSVDDLOYLGLL-YTFV 61

Db 6 FSYQENHSVSHNSFSEKNAQLAFEND-----DCHLPL-----AMFTLALAGAV 50

QY 62 SLIGFGNLLILMAKKRNQKTTVNFILGNLAFSDILVYLFCSPTFLTVSLDDQNNFGK 121

Db 51 IILGVSGNLLILILKQKEMRNVTNLIIVNLSFSDILVAVIMCPFFVYVTLDDHWGFE 110

QY 122 VMCHIMFLOCVSVLTVSLTILISIAIVRYHMIRKIPISNNLTANNGVYLITVNTLGAFC 181

Db 111 AMCKLNFVOCVSTIVTSFSLVLAVERHQLIINPKGRNNRHHAYGVIVYL--AVA 168

QY 182 SPLPVFHSVLQETFGSALLS---RYLCVESNPDSYRIAFITSLLYOYLPLVCLT 238

Db 169 SSLPFLYQWMTDEPFQNVTLDAKQKVOEDPSPSHSLSTTLTLVLYQYGPGLCFIF 228

QY 239 VSHRSVIRLKRNNRNMDDKRNKYSRSRSRYRLLTILVFAVSMPLHLFHYVTD 238

Db 229 ICYFKYIRLKRNNRNMDDKRNKYSRSSETRKINIMLSIVAFVACWMLPLTITFVFDW 288

QY 299 NDNLISNRHFKLVYVCICHLGMMSSCCNPLTYGFLNNGIRADL 341

Db 289 NQIATRCNNHNLFLCHLTAMISTCVNPIFYGLNKNFORDL 331

RESULT 9

NY1R_CAVPO STANDARD; PRT; 383 AA.

AC Q9WUD0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Neuropeptide Y receptor type 1 (NPY1-R).

GN NPY1R.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OC NCBI_TaxId=10141;

OX

RN

RP SEQUENCE FROM N.A.

RC MEDLINE=99427767; PubMed=10499421;

RX Berglund M.M., Holmberg S.K.S., Eriksson H., Gedda K., Maffrand J.-P., Serradeil-Le Gal C., Chhajlani V., Grundemar L., Larhammar D.;

```
RT "The cloned guinea pig neuropeptide Y receptor Y1 conforms to other
RT mammalian Y1 receptors."
PL Reptides 20:1043-1053(1999).
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL: AF135061; AAD43060.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 39
FT TRANSMEM 40 62
FT TRANSMEM 63 72
FT TRANSMEM 73 94
FT DOMAIN 95 114
FT TRANSMEM 115 136
FT DOMAIN 137 156
FT TRANSMEM 157 177
FT TRANSMEM 178 210
FT TRANSMEM 211 232
FT DOMAIN 233 263
FT TRANSMEM 264 286
FT DOMAIN 287 299
FT TRANSMEM 300 323
FT DOMAIN 324 383
FT CARBOHYD 2 2
FT CARBOHYD 11 11
FT CARBOHYD 17 17
FT DISULFID 113 198
FT LIPID 338 338
SQ SEQUENCE 383 AA; 44281 MW; E53BD93FAV35FE8 CRC64;

Query Match 34.9%; Score 640.5; DB 1; Length 383;
Best Local Similarity 37.8%; Pred. No. 6,2e-33;
Matches 130; Conservative 70; Mismatches 123; Indels 21; Gaps 5;

QY 2 SFPSKQDYNNMDELDEYNNKTATENNNTAATRNSDFPVMDYKSSVDDLYQFLGL-VTF 60
DB 5 SFQLEHNSHYNNSEKRPSEFAFEND-----DCHLPL-----AVFTLALAYGA 49
QY 61 VSLGFGNLLIIMALKRRKNOKTTVNFELIGNAFSDILVLFCSPTLTSVLLDDMMFG 120
DB 50 VIIIGVGNLALLIIIIKKQEMRNVTIILVNSFSDDLVAIMCLPTEVYTTLMHWIFG 109
QY 121 KVMCHMPFLQCVSVLTSLISIAIVRYHMKIPISNNLTANHGFLATVTLGFAI 180
DB 110 EIMCKLMPFQCVSIVSIFSLVLAVERHQLLINPRGWRNNHAIIGIAVIVL--AV 167
QY 181 CSPLPFVHSLVLEQETFGSALLSS--RYLCVESWPSDSRIAFTISLLLVQYTLPLVC 237
DB 168 ASSLPFWIYVLTDEPQNTVLTDAFKDKLVCFPDPSPDSHRLSYTTLTLVLYQCPICFI 227
QY 238 TVSHTSVICILKRRNNMMKMDKRRSSRSRYFRLTLLILVFNASWMPLIHFHVTD 297
DB 228 FICYFKIYILKRRNNMMDKRSKRSSESKRNIMLSIVAAFCWMLPTLTFNTVD 287
QY 298 FNDNLISNRHFKLVYCCILHGLGMMSCCLNPLILYGLNGIKADL 341
DB 288 MNHQIATACNHNLLFLCLHTAMISTCVNPIFGFLKNFQORDL 331

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RESULT 10
NR1_XENLA STANDARD; PRT; 366 AA.
AC P34992;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Neuropeptide Y receptor type 1 (NPY-R).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Mattens G.J.M., Blomqvist A.G., Roubos E.W., Larhammar D.;
RL Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHIKININS RECEPTORS.
-----
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DR EMBL: L25416; AAA49918.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 34
FT TRANSMEM 35 57
FT DOMAIN 58 67
FT TRANSMEM 68 89
FT DOMAIN 90 109
FT TRANSMEM 110 131
FT TRANSMEM 132 151
FT TRANSMEM 152 172
FT TRANSMEM 173 205
FT TRANSMEM 206 227
FT DOMAIN 228 258
FT TRANSMEM 259 281
FT DOMAIN 282 294
FT TRANSMEM 295 318
FT DOMAIN 319 366
FT CARBOHYD 2 2
FT CARBOHYD 9 9
FT CARBOHYD 15 15
FT CARBOHYD 181 181
FT DISULFID 108 193
FT LIPID 333 333
SQ SEQUENCE 366 AA; 42252 MW; B82C3C19A603FC67 CRC64;

Query Match 34.7%; Score 637; DB 1; Length 366;
Best Local Similarity 38.5%; Pred. No. 9,8e-33;
Matches 126; Conservative 71; Mismatches 120; Indels 10; Gaps 5;

QY 19 YNKLTATENNNTAATRNSDFPVMDYKSSVDDLYQFLGL-VTFVSLGFGNLLIIMALM 77
DB 6 YFENLSPNNISG--NTTFPISDCALPLP--MIFTLALAYGAVIIIGLSGNLALIIII 61
QY 78 KRRNQKTTVNFELIGNAFSDILVLFCSPTLTSVLLDDMMFGKVMCHMPFLQCVSVLV 137

```

DB      62 KQEMRWNTNILLVNSFSDLATIMCLPFTLLYTLMDHIFGEWCKLNEYIQCVSVTV
OY      138 STILISIAIVRYHMIKHPISNNLTANHGFLIATWATLGFALCSPLPVPHSIVELOETF
DB      122 STISVLVIAIERHOLLINPRGMRPNRRHACFGITVINGFMACTPLMAMSVLTD--EPF 179
OY      198 GSALLSS---RYLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVCIRLKRNNM 254
DB      180 KNISLDSYIGKYVCLDEDFEDKPRLSYTTLLFIQYLGCLFVFCYTKIFLRLKRNNM 239
OY      255 MCKMRNKRSSRSRSVRYTLTLLIVFANSMPLHFLHYVTFPNDNLISNRHFKLYCT 314
DB      240 MDKIRNKRSSSETKRINIMLSIVGFALCWLPEFLFNLVFPDMNEAVATCNHNLFLI 299
OY      315 CHLLGMSCCLPILYGLFNLNGIKADL 341
DB      300 CHLTAMISTCVNPFIYGFGLNKNFORDL 326

RESULT 11
NYIR.MOUSE      STANDARD:      PRT:      382 AA.
ID      NYIR.MOUSE
AC      004573; 061993;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Neuropeptide Y receptor type 1 (NPY1-R).
GN      NPY1R.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=93106169; PubMed=1468559;
RA      Eva C., Oberto A., Sprengel R., Genazzani E.;
RT      "The murine NPY-1 receptor gene. Structure and delineation of tissue-
RT      specific expression.";
RL      FEBS Lett. 314:285-288(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96102072; PubMed=8530415;
RA      Nakamura M., Sakana C., Aoki Y., Ogasawara H., Tsuji T.,
RA      Kodama H., Matsumoto T., Shimizu T., Noma M.;
RT      "Identification of two isoforms of mouse neuropeptide Y-Y1 receptor
RT      generated by alternative splicing. Isolation, genomic structure, and
RT      functional expression of the receptors.";
RL      J. Biol. Chem. 270:30102-30110(1995).
CC      -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: NPY1-R ALPHA (SHOWN HERE) AND
CC      NPY1-R BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: THE ALPHA FORM IS HIGHLY EXPRESSED IN THE
CC      BRAIN, HEART, KIDNEY, SPLEEN, SKELETAL MUSCLE, AND LUNG, WHEREAS
CC      THE BETA RECEPTOR MRNA WAS NOT DETECTED IN THESE TISSUES. HOWEVER,
CC      THE BETA FORM IS EXPRESSED IN MOUSE EMBRYONIC DEVELOPMENTAL STAGE
CC      (7 AND 11 DAYS), BONE MARROW CELLS AND SEVERAL HEMATOPOIETIC CELL
CC      LINES.
CC      -1- DEVELOPMENTAL STAGE: THE BETA FORM IS EXPRESSED IN EMBRYONIC
CC      DEVELOPMENTAL STAGE (7 AND 11 DAYS). THE BETA FORM IS AN EMBRYONIC
CC      AND A BONE MARROW FORM OF NPY1-R, WHICH DECREASES IN THE
CC      EXPRESSION DURING DEVELOPMENT AND DIFFERENTIATION.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      HIGHEST TO TACHYKININS RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/

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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: 218280; CAA79157.1;
DR      EMBL: 218281; -: NOT_ANNOTATED_CDS.
DR      EMBL: D63818; BAA09887.1;
DR      EMBL: D63819; BAA09888.1;
DR      PIR: S27388; S27388.
DR      MGD: MG1:104963; NPY1r.
DR      InterPro: IPR000276; GPCR_Rhodopsin.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1;
DR      PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; glycoprotein;
KW      Phosphorylation; Lipoprotein; Palmitate; Alternative splicing.
FT      DOMAIN 1
FT      TRANSMEM 39..61
FT      DOMAIN 2
FT      TRANSMEM 62..71
FT      TRANSMEM 72..93
FT      DOMAIN 3
FT      TRANSMEM 94..113
FT      TRANSMEM 114..135
FT      DOMAIN 4
FT      TRANSMEM 136..155
FT      TRANSMEM 156..176
FT      DOMAIN 5
FT      TRANSMEM 177..209
FT      TRANSMEM 210..231
FT      DOMAIN 6
FT      TRANSMEM 232..262
FT      TRANSMEM 263..285
FT      DOMAIN 7
FT      TRANSMEM 286..298
FT      TRANSMEM 299..322
FT      DOMAIN 8
FT      TRANSMEM 323..382
FT      CARBOHYD 2
FT      CARBOHYD 11
FT      CARBOHYD 17
FT      CARBOHYD 112
FT      DISULFID 112..197
FT      LIPID 337..337
FT      VARSPIC 304
FT      VARSPIC 308
FT      VARSPIC 382
SQ      SEQUENCE 382 AA; 44014 MW; CDCCF93E3ABABD70 CRC64;

Query Match      34.5%; Score 633.5; DB 1; Length 382;
Best local Similarity 37.8%; Pred. No. 1,7e-32;
Matches 127; Conservative 73; Mismatches 115; Indels 21; Gaps 6;

OY      20 NKTLL--ATENNTA--ATRNSDPEVMDYKSSVDLQYFLIGLYTF-----VSLGFMG 68
DB      2 NSTLFSVEVHSHYNASENSPLAFEN-----DDCHLPLAVIFTLALAVAGVILLGVSG 56
OY      69 NLILALMKRRKQKTVNFLIGNLAESDLVLFCSPTFLTSVLDQMGFKVMCHIMP 128
DB      57 NLALIIILIKQEKERNVTNILLVLSFSDLLVAVMCIPFEVYVTLMDHWFGEFMCKLNP 116
OY      129 FLOCVSVLSTLLISIAIVRYHMIKHPISNNLTANHGFLIATWATLGFALCSPLPVPFH 188
DB      117 FVCCSVLTSVLSVLVLAVERHOLLINPRGMRPNRRAYIGITVIAVLAASSLPEVITYQ 176
OY      189 SVELOETFGESALLSS---RYLCVESWPSDSYRIAFITSLLYOYLPLVCLTVSHTSVC 245
DB      177 ILND--EPFNWLSAKFKDXYVCDKRPDSHRSYSTLLVLVIGYRPLCFIFCYKIV 234
OY      246 IRLKRRNNMCKMRNKRSSRSVRYTLTLLIVFANSMPLHFLHYVTFPNDNLISNRHFKLYCT 305
DB      235 IRLKRRNNMCKMRNKRSSRSVRYTLTLLIVFANSMPLHFLHYVTFPNDNLISNRHFKLYCT 294
OY      306 RHFKLYVCIHLLGMSCCLPILYGLFNLNGIKADL 341
DB      295 CNHNLLELCHLTAMISTCVNPFIYGFGLNKNFORDL 330

RESULT 12
NYIR.RAT      STANDARD:      PRT:      382 AA.
ID      NYIR.RAT
AC      P21555;
DT      01-MAY-1991 (Rel. 18, Created)

```

DT 01-MAY-1992 (Rel. 22, last sequence update)
 DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE Neuropeptide Y receptor type 1 (NPY1-R) (FC5).
 GN NPY1R.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91032093; PubMed=2172008;
 RA Eva C., Keisänen K., Møyer H., Seeburg P.H., Sprengel R.;
 RT "Molecular cloning of a novel G protein-coupled receptor that may
 RT belong to the neuropeptide receptor family.";
 RL FEBS Lett. 271:81-84(1990).
 RN [2]
 RP REVISIONS, AND FUNCTION.
 RC TISSUE=Brain;
 RA Krause J.E., Eva C., Seeburg P.H., Sprengel R.;
 RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO TACHYKININS RECEPTORS.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL: Z11504; CAAT7579.1; -.
 DR PIR: S12863; S12863.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 38
 FT TRANSMEM 39 61
 FT DOMAIN 62 71
 FT TRANSMEM 72 93
 FT DOMAIN 94 113
 FT TRANSMEM 114 135
 FT DOMAIN 136 155
 FT TRANSMEM 156 176
 FT DOMAIN 177 209
 FT TRANSMEM 210 231
 FT DOMAIN 232 262
 FT TRANSMEM 263 285
 FT DOMAIN 286 298
 FT TRANSMEM 299 322
 FT DOMAIN 323 382
 FT CARBOHYD 2
 FT CARBOHYD 11 11
 FT CARBOHYD 17 17
 FT DISULFID 112 197
 FT LIPID 337 337
 FT SEQUENCE 382 AA; 44116 MW; ID6AA038065C07C3 CRC64;

 Query Match 34.5%; Score 633.5; DB 1; Length 382;
 Best local similarity 38.5%; Pred. No. 1,7e-32;
 Matches 121; Conservative 71; Mismatches 116; Indels 6; Gaps 3;

 QY 32 TRNSDPVWDYKSSVDLQYFLIGL-YTFVSLGFMGNLLIMALKKRNOKTTFELI 90
 Db 19 SENSPLAFENDCHPLAVIVFTLALAYGAVIILTSVSGNLAIIIIILKKEMKRVNII 78

QY 91 GNLAESDILVVFCSPEFLTSVLDQMMFGKVMCHIMEPLQCVSLVSTLLISAIIVR 150
 Db 79 VNLSESDLLVAVMCLPFFVYTLMDHWFGEMCKLNFPQCVSTVTSIFSLVLAVERH 138
 QY 151 HMKIPISNNLTANNGYFLATVWTFLGPAICSPLVEFHSVLVELOFTSALISS---RYL 207
 Db 139 QLTINRCGRPNRNHAYIGIVIWLAFAVSSLPFVIYQILND--EPFQNVSLAAFKDKYV 196
 QY 208 CVESWPSDSYRIAFITSLIVQYILPLVCLFVSHSVICRLKRNNMMDKMRNKRSSR 267
 Db 197 CFDRFPSSHRLSTTLVLQYREPLCFITCYIKIIRLKRNNMMDKIRDSKYSSE 256
 QY 268 SRSVFYRITLILVFAVSMPLHLFHVYTFDNDMLISNRHKEVYCICHLGMSSCLNP 327
 Db 257 TKRINVMLLSIVFAVACWMLPLTFITFNVEDMNHQIATCNHLLFLCHLTAMISTCVNP 316
 QY 328 ILVGFNLNGIRADL 341
 Db 317 IFYGLNKNFORDL 330

 RESULT 13
 ID N6R_RABIT STANDARD: PRT; 371 AA.
 AC P79217;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE Neuropeptide Y receptor type 6 (NPY6-R).
 GN NPY6R.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Skeletal muscle;
 RX MEDLINE=97066888; PubMed=8910290;
 RA Matsunoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiko H.,
 RA Rogami J., Kimura Y., Okada M., Yamaguchi T.;
 RT "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in
 RT primate species.";
 RL J. Biol. Chem. 271:27217-27220(1996).
 CC -1- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
 CC CYCLASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO TACHYKININS RECEPTORS.

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 CC or send an email to license@isb-sib.ch).

 DR EMBL: D66521; BAA13104.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 34
 FT TRANSMEM 35 57
 FT DOMAIN 58 69
 FT TRANSMEM 70 90
 FT DOMAIN 91 110
 FT TRANSMEM 111 132

QY 191 VELOETGSSALLSRVLCVESPSDYRIAFITSLIVQYILPLVCLVSHTSVCIRLR 250
 Db 184 -----SLEPTDYTHQVACWEIWPSPKLNQLFSTSLFMLOYVPLGFIILICYLKLCKLR 238
 QY 251 RNNMMDKMRDKYRSSRSRYEYRLTILILEVAWSMPLH.FHVVYTDENDNISRRHKL 310
 Db 239 RTROYDRKREKRSRLNEKRKNVNLISIVTFGACMLPLNTFNVLFDWYHEKLSCHHDL 298
 QY 311 VYCIHLLGMSCCLNPLLYGLFNLNGIKADIVSLIH 346
 Db 299 VFVVCILIAMVSTCINPLFYGLFNKNFKQDLMLILH 334

RESULT 15
 NY2R.CHICK
 ID NY2R.CHICK STANDARD: PRT: 385 AA.
 AC Q9DDN6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
 GN NPY2R.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20532533; Pubmed-11078884;
 RA Salaneck E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D.;
 RT "Chicken neuropeptide Y receptor Y2: structural and pharmacological
 RL differences to mammalian Y2.";
 RL FEBS Lett. 484:229-234(2000).
 CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- HIGHEST TO TACHYKININS RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF309091; AAG37898.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 53
 FT TRANSMEM 54 76
 FT DOMAIN 77 86
 FT TRANSMEM 87 108
 FT DOMAIN 109 128
 FT TRANSMEM 129 150
 FT DOMAIN 151 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 218
 FT TRANSMEM 219 244
 FT DOMAIN 245 272
 FT TRANSMEM 273 295
 FT DOMAIN 296 308
 FT TRANSMEM 309 332
 FT DOMAIN 333 385
 FT CARBOHYD 11 11
 FT DISULFID 127 207
 FT LIPID 346 346
 FT PALMITATE (POTENTIAL).

SQ SEQUENCE 385 AA; 43509 MW; 60A09B314E665B62 CRC64;
 Query Match 28.6%; Score 525; DB 1; Length 385;
 Best Local Similarity 32.6%; Pred. No. 7,66-26;
 Matches 99; Conservative 75; Mismatches 116; Indels 14; Gaps 4;
 QY 49 DLQYFLGLYFVSVILGFMGMLILMALMKRNOKTYVNFILGNLAFSDIIVLECSPT 108
 Db 52 EVQILIRAVCSIIILGIVGNSLVTHVILIKFSMRTVNFPIANLAVADLLVNTLCLEPT 111
 QY 109 LFSVLLDQMMRGKVMCHIMPFLQCVSVLSTLLISTAIIVRYHMKHPIISNNLANHGYF 168
 Db 112 LVYTLGEMKLGPVLCILVPYQAQALAVHSTVTLTVALDLDRRCIVHLESKISKISFEL 171
 QY 169 LIATVWTGFAICSPLPVF--HSLVELOETGSSALLSRVLCVESPSD--SYRIAFIT 223
 Db 172 IIGVAMAVSALLASPLAFREXSLILEIPDF-----KIYVCEKWPREGQLNGTIVSV 225
 QY 224 SILLVQYILPLVCLVSHTSVCIRLKRNNMMDKMRDKYRSSRSRYEYRLTILILEVA 283
 Db 226 SMLLIQYVLPALISVAYTRIMTKL--NHVSPGAGNDHYHHRQKTKMLVCVVVFA 282
 QY 284 VSNMPLHFHVYTDENDNLISNRHFKLYVYCIHLLGMSCCLNPLLYGLFNLNGIKADIVS 343
 Db 283 VSMLEPFAFQVLVDISQVLDLKEKLYIVFVHIAMCSTFANPLLYGMNNNRYTAFLT 342
 QY 344 LIHC 347
 Db 343 AFQC 346

Search completed: November 22, 2002, 13:09:44
 Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:24 ; Search time 21 Seconds
(without alignments)
1602.240 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836
Sequence: 1 MSFYSKQDYNMDELDEYYN.....GFLNNGIKADVLILHCLHM 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	35.1	384	2 A45490	neuropeptide Y/pep
2	637	34.7	366	2 S71152	neuropeptide Y/pep
3	633.5	34.5	349	2 S12863	G protein-coupled
4	633.5	34.5	382	2 S27388	neuropeptide Y rec
5	633.5	34.5	382	2 B46133	neuropeptide Y/pep
6	515.5	28.1	375	2 S63685	neuropeptide Y rec
7	515	28.1	375	2 I39182	neuropeptide Y/pep
8	514	28.0	375	2 G02300	pancreatic polypep
9	504	27.5	381	2 I39187	neuropeptide Y/pep
10	453.5	24.7	370	1 I52315	G protein-coupled
11	421.5	23.0	449	2 A41738	neuropeptide Y rec
12	397.5	21.7	455	2 T15622	hypothetical prote
13	365.5	19.9	423	2 B40470	glucocorticoid-ind
14	362	19.7	412	2 T22076	hypothetical prote
15	358.5	19.5	436	2 JCS599	cholecystokinin-A
16	357	19.4	365	2 T20184	hypothetical prote
17	356.5	19.4	427	2 S50150	gastric CCK-A rece
18	354	19.3	444	2 A42685	hypothetical prote
19	345.5	18.8	399	2 T16277	hypothetical prote
20	345.5	18.8	443	2 D40470	glucocorticoid-ind
21	344.5	18.8	349	2 I59336	galanin receptor 1
22	344	18.7	423	2 JCS677	allatostatin recep
23	341	18.6	357	2 JCS719	probable allatosta
24	341	18.6	430	2 I51898	cholecystokinin A
25	340.5	18.5	391	2 T132714	hypothetical prote
26	340	18.5	398	1 J01059	neurokinin 2 recep
27	336.5	18.3	428	2 JN0692	cholecystokinin ty
28	335	18.2	394	2 JCS709	galanin receptor -
29	334.5	18.2	584	2 JCS7809	sulfakinin recepto

30	332	18.1	457	2 T29741	hypothetical prote
31	327.5	17.8	384	1 S00516	neurokinin 2 recep
32	324	17.6	402	2 I56595	neurokinin 2 recep
33	323	17.6	374	2 T19340	hypothetical prote
34	322	17.5	452	2 A46195	cholecystokinin B
35	321.5	17.5	491	2 C40470	glucocorticoid-ind
36	321	17.5	390	2 B88684	protein ACT.1 (lmp
37	320	17.4	416	2 T30946	hypothetical prote
38	317	17.3	384	2 I57957	neurokinin 2 recep
39	316.5	17.2	539	2 T27559	hypothetical prote
40	312.5	17.0	384	2 S20303	neurokinin 2 recep
41	312.5	17.0	519	2 S17783	tachykinin recepto
42	312	17.0	384	2 A41007	gastrin-releasing
43	311.5	17.0	407	2 S20304	neurokinin 1 recep
44	311	16.9	453	2 S32817	gastrin receptor -
45	310.5	16.9	376	2 T19186	hypothetical prote

ALIGNMENTS

RESULT 1
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C:Accession: A45490; A46133; A42773
R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Cross-references: GB:I07615; NID:9189284; PIDN:AA45947.1; PID:9189285
A:Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBI:128005)
R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messeng
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: A46133
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-384 <HER>
A:Note: sequence extracted from NCBI backbone (NCBIP:108538)
R:Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlstedt, C.
J. Biol. Chem. 267, 10935-10938, 1992
A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY recep
A:Reference number: A42773; MUID:92283782; PMID:1317848
A:Accession: A42773
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LAR>
A:Cross-references: GB:M88461; NID:9189155; PIDN:AAA73215.1; PID:9189156
A:Note: preliminary source: fetal brain
A:Experimental source: fetal brain
A:Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBIP:104736)
C:Genetics:
A:Gene: GDB:NPYR; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-4q32
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolest
F:37-66/Domain: transmembrane #status predicted <TM1>
F:77-103/Domain: transmembrane #status predicted <TM2>
F:118-136/Domain: transmembrane #status predicted <TM3>
F:155-179/Domain: transmembrane #status predicted <TM4>
F:209-232/Domain: transmembrane #status predicted <TM5>
F:261-286/Domain: transmembrane #status predicted <TM6>
F:300-323/Domain: transmembrane #status predicted <TM7>
F:113-198/Disulfide bonds: #status predicted
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 35.1%; Score 644; DB 2; Length 384;
Best Local Similarity 37.9%; Pred. No. 6.4e-45;
Matches 130; Conservative 70; Mismatches 122; Indels 21; Gaps 5;

QY 3 FYSKDYMMDELDEYYNKTLATENNATRNSPVDDYKSSVDDLOQYFLIGL-YTFV 61
D 6 FSOVENHVSVHSNFSKMQLLAFEND-----DCHPLP-----AMIFLALAYCAV 50
QY 62 SLGFMGULLIMALKRNRKQTYNPLGLNLSFDILVLFCSPTLTSLVDQMMFGK 121
D 51 IILGSGMLALLIILKOKEMRNNTLIVNLSFSDLLVAILMCLPFTFVYTLMDHWGCE 110
QY 122 VMCHIMPLQCVSVLSTLILISIAIVRYHMIKHPISNNLTAHNGYFLIATVTLTGFAIC 181
D 111 AMCKINPFOVCSTIVSTFSLVLAVERRHOLINRGRRPNRRHAYGIAVITWL--AVA 168
QY 182 SPLPVHSLVELQETFGSALLS---RYLCVESWPSDSYRIAFITSLILVQYILPVLCT 238
D 169 SSLPFLIYQVMTDEPQVWTLDAVKDYVCFDQPSDSHRLSYTTLVLLVQYFGPLCFIF 228
QY 239 VSHRSVCIKRLRRNMMDKMDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDF 298
D 229 ICYKRIYRLKRRNMMDKMDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDF 298
QY 299 NDNLISNHFRLVYICICHLGMSCLPILYGFNLNGIKADL 341
D 289 NHOIATCNHNLFLCHLTAMISTCVNPIFYGLNKNFQDRL 331

RESULT 2
571152
neuropeptide Y/peptide YY receptor Y1 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
C:Accession: S71152; S55924
R:Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.
Submitted to the EMBL Data Library, November 1993
A:Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xeno
A:Reference number: S71152
A:Accession: S71152
A:Molecule type: mRNA
A:Residues: 1-366 <MAR>
A:Cross-references: EMBL:L25416; NID:9409169; PIDN:AAA49918.1; PID:9409170
A:Experimental source: brain, hypothalamus
R:Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.
Biochim. Biophys. Acta 1261, 439-441, 1995
A:Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA f
A:Reference number: S55924; MUID:95260870; PMID:7742373
A:Accession: S55924
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-278, 'T', 280-366 <BLD>
A:Cross-references: EMBL:L25416; NID:9409169
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 34.7%; Score 637; DB 2; Length 366;
Best Local Similarity 38.5%; Pred. No. 2.2e-44;
Matches 126; Conservative 71; Mismatches 120; Indels 10; Gaps 5;

QY 19 YNKTLATENNATRNSPVDDYKSSVDDLOQYFLIGL-YTFVSLGFMGULLIMALKM 77
D 6 YFENLSVNNISG--NITPFISEDCALPLP--MIFLALAYCAVAILIGLSNGLALIIIL 61
QY 78 KRNQKQTVVFLIGNLAFSDILVLFCSPTLTSLVDQMMFGKVMCHIMPLQCVSVL 137
D 62 KOKEMRNNTLIVNLSFSDLLVAILMCLPFTFVYTLMDHWGCEVYTLMDHWGCE 121
QY 138 STILISIAIVRYHMIKHPISNNLTAHNGYFLIATVTLTGFAICSPILPVHSLVELQET 197
D 122 STISVLIAIERHOLINRGRRPNRRHAYGIAVITWL--AVA 168
QY 198 GSALLS---RYLCVESWPSDSYRIAFITSLILVQYILPVLCTVSHRSVCIKRLRRNM 254

Db 160 KNISLDSYIGKYVCEDEPEDEKFRILSYTTLFLIOLYGLPCLFICYCYKIFRLKRRNM 239
QY 255 MDKMRDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDFNDNLISNHFRLVYCI 314
D 240 MDKIDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDFNDNLISNHFRLVYCI 314
QY 315 CHLGMSCCLNPIILYGFNLNGIKADL 341
D 300 CHLTAMISTCVNPIFYGLNKNFQDRL 326

RESULT 3
S12863
G protein-coupled receptor FC5 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Apr-2000
C:Accession: S12863; S19101
R:Eva, C.; Kelnanen, K.; Mønyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A:Title: Molecular cloning of a novel G protein-coupled receptor that may belong to t
A:Reference number: S12863; MUID:91032093; PMID:2172008
A:Accession: S12863
A:Molecule type: mRNA
A:Residues: 1-349 <EVA>
A:Cross-references: EMBL:211504
R:Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
Submitted to the EMBL Data Library, November 1991
A:Description: Pharmacological and Transduction Properties of a Recombinantly Express
A:Reference number: S19101
A:Accession: S19101
A:Molecule type: mRNA
A:Residues: 1-343; 'DYEITANSTMHTDYSKTSLKQASPAVKRISMDNERT' <KRA>
A:Cross-references: EMBL:211504; NID:957636; PIDN:CAA7579.1; PID:957637
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:39-61/Domain: transmembrane #status predicted <TM1>
F:73-93/Domain: transmembrane #status predicted <TM2>
F:114-135/Domain: transmembrane #status predicted <TM3>
F:155-175/Domain: transmembrane #status predicted <TM4>
F:213-231/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:299-322/Domain: transmembrane #status predicted <TM7>
F:2.11.17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 34.5%; Score 633.5; DB 2; Length 349;
Best Local Similarity 37.8%; Pred. No. 4.1e-44;
Matches 127; Conservative 72; Mismatches 116; Indels 21; Gaps 6;

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D 2 NSTLFSRVENVSVHYNSSENSFLAFEN-----DCHPLPVLAVITLALAYCAVAILIGVSG 56
QY 69 NLIILMALKRNRKQTYNPLGLNLSFDILVLFCSPTLTSLVDQMMFGKVMCHIM 128
D 57 NLAIIILKOKEMRNNTLIVNLSFSDLLVAILMCLPFTFVYTLMDHWGCEVYTLMDHWGCE 116
QY 129 FLOCVSVLSTLILISIAIVRYHMIKHPISNNLTAHNGYFLIATVTLTGFAICSPILPVH 188
D 117 FVOCSTIVSTFSLVLAVERRHOLINRGRRPNRRHAYGIAVITWLAVASSLPVYIYQ 176
QY 189 SLVELQETFGSALLS---RYLCVESWPSDSYRIAFITSLILVQYILPVLCTVSHRSV 245
D 177 ILTD--EPFQNVSLAFAFKDYVCFDQPSDSHRLSYTTLVLLVQYFGPLCFIFCYCFKI 234
QY 246 IRLKRRNMMDKMDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDFNDNLISN 305
D 235 IRLKRRNMMDKMDNKRSSRSVFRLLIILVFAVSMPLHLHVVTDFNDNLISN 305
QY 306 RHFKIYVCIHLGMSCLNPIILYGFNLNGIKADL 341
D 295 CNHNLFLCHLTAMISTCVNPIFYGLNKNFQDRL 330

RESULT 4
S27388
neuropeptide Y receptor NPY-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
C:Accession: S27388
R:Eva, C.; Oberio, A.; Sprengel, R.; Genazzani, E.
FEBS Lett. 314, 285-288, 1992
A:Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex
A:Reference number: S27388; MUID:93106169; PMID:1468559
A:Accession: S27388
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <EVA>
A:Cross-references: EMBL:Z18280; NID:953438; PIDN:CAA79157.1; PID:953439
C:Superfamily: neurokinin 1 receptor

Query Match 34.5%; Score 633.5; DB 2; Length 382;
Best Local Similarity 37.8%; Pred. No. 4.5e-44;
Matches 127; Conservative 73; Mismatches 115; Indels 21; Gaps 6;

QY 20 NKTLP--ATENNTA---ATRSDFPVMDDYKSSVDDLYFLGLYTF-----VSLGFMG 68
DB 2 NSTLFSKVENHSHYNASENSPLAFEN---DDCHLPLAVIFTLALAYGAVILILGVSG 56
QY 69 NLILALMKRRNOKTVNFIENLAFSDILVLFCSPEFTLSVLLDQMMFGKVMCHIMP 128
DB 57 NLALIIILIKOKEMRNVNLIIVLVSFSDILVAVMCPLPFTFVYTLMDHWVFGEMCKLNP 116
QY 129 FLOCVSVLSTLILISIAIVRYHMIKIPISNNLTANHGYELIATVWTLGFAICPLPVEH 188
DB 117 FVOCSTIVTAFISFLIVLAVRHOILINPGRWPRNNRHAYIGITVIVLAVASSLPFVY 176
QY 189 SIVLEQTFGSALLS---RYLCESWPSDSYRIAFITSLILVQYILIPCYLTVSHSYC 245
DB 177 ILVD--EPFQNSLSLAARKDYVCDFKPSDSHRLSYTTLVLQYFGPLCFIFCYKRY 234
QY 246 IRLKRRNNMMDKMRDNKRYRSRSRYRFLTILILVFAVSMPLPHLPHVYTDENDLISN 305
DB 235 IRLKRRNNMMDKIRDSKYRSEETKRINIMLSIYAVAVCMPLTITNTVYFDNMHQIAT 294
QY 306 RHEKLYVCICHLGMMSCCLNPILYGFLLNGIKRADL 341
DB 295 CNHMLFLCHLTAMISTCVNPILFYGLKNKFORDL 330

RESULT 5
B46133
neuropeptide Y/peptide YY receptor Y1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C:Accession: B46133
R:Herzog, H.; Holt, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: B46133
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-382 <HER>
A:Note: sequence extracted from NCBI backbone (NCBIP:108539)
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 34.5%; Score 633.5; DB 2; Length 382;
Best Local Similarity 38.5%; Pred. No. 4.5e-44;
Matches 121; Conservative 71; Mismatches 116; Indels 6; Gaps 3;

QY 32 TRNSDFPVMDDYKSSVDDLYFLGLYTFVSLGFMGNLILALMKRRNOKTVVFLI 90
DB 19 SENSPLAFENDCHLPLAVIFTLALAYGAVIILGVSGNLALIIILIKOKEMRNVNILI 78

QY 91 GNLAESDILVLFCSPTLTSVLLDQMMFGKVMCHIMPLOCVSVLSTLILISIAIVRY 150
DB 79 VNLSFSDILVAVCMCLPFTFVYTLMDHWVFGEMCKLNPFOCVSITVIFSLVIAVERH 138
QY 151 HMIKIPISNNLTANHGYELIATVWTLGFAICSPLPVHSHLVEQTFGSALLS---RYL 207
DB 139 QLIINPGRWPRNNRHAYIGITVIVLAVASSLPFVYQILTD--EPFQNSLSLAARKDY 196
QY 208 CVESWPSDSYRIAFITSLILVQYILIPCYLTVSHSYCIRLKRNNMMDKMRDNKRYRSR 267
DB 197 CFKFPDSHRLSTTILVLQYHGFPLCFIFCYKRYIRLKRNNMMDKIRDSKYSSSE 256
QY 268 SRSVYRRLTILILVFAVSMPLPHLPHVYTDENDLISNRHFKLYVCICHLGMMSCCLNP 327
DB 257 TKRINWLLSIVAFVAVCMPLPFTFNTVFDNMHQIATCNHMLFLCHLTAMISTCVNP 316
QY 328 ILVGFLLNGIKRADL 341
DB 317 IFYGLKNKFORDL 330

RESULT 6
S63685
neuropeptide Y receptor D type - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
C:Accession: S63685
R:Gregor, P.; Millham, M.L.; Feng, Y.; Decarr, L.B.; McCallieb, M.L.; Cornfield, L.J.
FEBS Lett. 381, 58-62, 1996
A:Title: Cloning and characterization of a novel receptor to pancreatic polypeptide,
A:Reference number: S63685; MUID:96193913; PMID:8641440
A:Accession: S63685
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <GRE>
A:Cross-references: EMBL:U040189; NID:91223969; PIDN:AA052442.1; PID:91223970
C:Superfamily: neurokinin 1 receptor

Query Match 28.1%; Score 515.5; DB 2; Length 375;
Best Local Similarity 32.9%; Pred. No. 1.7e-34;
Matches 103; Conservative 66; Mismatches 119; Indels 23; Gaps 5;

QY 49 DLOYFLGLYTFVSLGFMGNLILALMKRRNOKTVNFIENLAFSDILVLFCSPT 108
DB 39 ELAFLITTYSIETILGLVGLICLIETTRQKESVNTNLILANLARSDFLMCLICQPLT 98
QY 109 LTSVLLDQMMFGKVMCHIMPLOCVSVLSTLILISIAIVRYHMIKIPISNNLTANHGYF 168
DB 99 VTYTIMDYWIFGEVLCMKLTFIQMSVTSILSLVALERHOLIINPTGMRKPSIFQAYL 158
QY 169 LIATVWTLGFAICSPPL-----PVFH-----SLVEQTFGSALLSRYLCVESWPSDSY 217
DB 159 GIIVYVIFSCFLSLPFLANSTLNDLFYHNSKVE-----FLEDKVVCFSWSSDHH 210
QY 218 RIAFTISILVQYILIPCYLTVSHSYCIRLKRNNMMDKMRDNKRYRSRSRYRFLTI 277
DB 211 RLATYTFLLFYOCIRPLAFILVYCIIRYGLRQKRGVFNHACSS--RAGMKRINSLMT 269
QY 278 LILVFAVSMPLPHLPHVYTDENDLISNRHFKLYVCICHLGMMSCCLNPILYGLFLLNGI 337
DB 270 MYTAAFAVLMPLPHVFNTEDEMYGEAIPACHGNLIFLMCHILMAASTCVNPFYIGFLINP 329
QY 338 KADVSLI---HC 347
DB 330 KDKIKALVLTCHC 342

RESULT 7
I39182
neuropeptide Y/peptide YY receptor Y4 - human
C:Species: Homo sapiens (man)
C>Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000


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OY 143 ISIAIVRYHMKHPISNNL--TANHGYPILATVWTLGFAICSPLPVHSLVELQETGSA 200
    :|:| | | : : : | :| | | | :|:|:| |
Db 133 VAISLERGALCRPLQSRVQTKSHALKYIAATWCLSETIMTPYISNLPFTKNNQI 192
    :|:| | | : : : | :| | | | :|:|:| |
OY 201 LLSRYLCVESMPDSYRIAFITISLLVOYILPLVCLTVSHTSVCIRL-----KRRN 252
    :|:| | | : : : | :| | | | :|:|:| |
Db 193 ANMGRFLL-----PSDAMQOSWOTFLLLILFLIPGVWVVAIGLISLELYOGIKFDASOKK 248
    :|:| | | : : : | :| | | | :|:|:| |
OY 253 NMMDKM-----RDNKYRSSR 267
    :|:| | | : : : | :| | | | :|:|:| |
Db 249 SAKKRLSSGGGGSSSSRVEDSGCYLQKSNRPKRLELQJLSTSSSGRINRIRSSG 308
    :|:| | | : : : | :| | | | :|:|:| |
OY 268 S-----RSYFRLTILILVEAVSMPLHLEHVYTDPNNDLISNRHK---LVYCICHL 317
    :|:| | | : : : | :| | | | :|:|:| |
Db 309 SAANLIARKRYIRMLIVIVLFFLCWMPIFSANAMRAY-DTWSAEKHLSCGPISFIL--L 365
    :|:| | | : : : | :| | | | :|:|:| |
OY 318 LGMSCCLNPLTYGLNNGIKADLVSLIHC 347
    :|:| | | : : : | :| | | | :|:|:| |
Db 366 LSTYSSCVNPLIYCENKRRRLGFMATPPC 395
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Search completed: November 22, 2002, 13:10:52
 Job time : 23 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:09:29 ; Search time 10 Seconds

(without alignments)
548.152 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836
Sequence: 1 MSFYSKODYNMDELDEYYN.....GFLNNGKADVLHCLHM 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1836	100.0	350	10	US-09-771-956-6 Sequence 6, Appl
2	1777	96.8	394	10	US-09-771-956-10 Sequence 10, Appl
3	1743	94.9	341	10	US-09-771-956-20 Sequence 20, Appl
4	1699	92.5	341	10	US-09-771-956-26 Sequence 26, Appl
5	1693	92.2	383	10	US-09-771-956-21 Sequence 21, Appl
6	1691	92.1	352	10	US-09-771-956-23 Sequence 23, Appl
7	1668.5	90.9	455	10	US-09-771-956-13 Sequence 13, Appl
8	1668.5	90.9	455	10	US-09-962-646-4 Sequence 4, Appl
9	1665.5	90.7	455	10	US-09-771-956-30 Sequence 30, Appl
10	1647	89.2	383	10	US-09-771-956-27 Sequence 27, Appl
11	1637	89.2	395	10	US-09-771-956-25 Sequence 25, Appl
12	1609.5	87.7	499	10	US-09-771-956-9 Sequence 9, Appl
13	1536	83.7	456	10	US-09-962-646-2 Sequence 2, Appl
14	1482	80.7	499	10	US-09-771-956-24 Sequence 24, Appl
15	1461.5	79.6	508	10	US-09-962-646-22 Sequence 22, Appl
16	1025.5	55.9	334	10	US-09-962-646-6 Sequence 6, Appl
17	644	35.1	384	10	US-09-771-956-2 Sequence 2, Appl
18	638	34.7	384	10	US-09-962-646-15 Sequence 15, Appl
19	633.5	34.5	382	10	US-09-771-956-3 Sequence 3, Appl

20	515	28.1	375	10	US-09-962-646-17 Sequence 17, Appl
21	504	27.5	381	10	US-09-962-646-16 Sequence 16, Appl
22	504	27.5	381	10	US-09-292-973-5 Sequence 5, Appl
23	504	27.5	381	10	US-09-292-973-20 Sequence 20, Appl
24	479	26.1	227	12	US-10-044-592-69 Sequence 69, Appl
25	464	25.3	370	12	US-10-044-592-12 Sequence 12, Appl
26	464	25.3	370	12	US-10-044-592-74 Sequence 74, Appl
27	429	23.4	518	10	US-09-804-551B-8 Sequence 8, Appl
28	415.5	22.6	522	10	US-09-804-551B-38 Sequence 38, Appl
29	378.5	20.6	423	8	US-08-796-570A-1 Sequence 1, Appl
30	378.5	20.6	423	9	US-10-067-477-1 Sequence 1, Appl
31	375	20.4	540	10	US-09-804-551B-2 Sequence 2, Appl
32	367	20.0	428	10	US-09-292-973-4 Sequence 4, Appl
33	366.5	20.0	426	10	US-09-292-973-19 Sequence 19, Appl
34	366.5	20.0	432	10	US-09-292-973-2 Sequence 2, Appl
35	357.5	19.5	431	10	US-09-826-508-22 Sequence 22, Appl
36	357.5	19.5	431	10	US-09-899-532-2 Sequence 2, Appl
37	333	18.1	427	10	US-09-730-931-2 Sequence 2, Appl
38	328	17.9	223	12	US-10-044-592-72 Sequence 72, Appl
39	326	17.8	223	12	US-10-044-592-71 Sequence 71, Appl
40	321	17.5	402	12	US-10-077-874-2 Sequence 19, Appl
41	321	17.5	425	10	US-09-828-538-19 Sequence 19, Appl
42	321	17.5	425	10	US-09-828-538-24 Sequence 24, Appl
43	321	17.5	425	10	US-09-961-848-2 Sequence 2, Appl
44	318	17.3	372	12	US-10-077-874-6 Sequence 6, Appl
45	317.5	17.3	389	10	US-09-828-538-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-771-956-6
; Sequence 6, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Benmett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA
US-09-771-956-6

Query Match 100.0%; Score 1836; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.1e-145;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSKODYNMDELDEYYNKTATENNATRRSDPPVDDYKSSVDDQYFLIGLYTF 60
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Db 1 MSFYSKODYNMDELDEYYNKTATENNATRRSDPPVDDYKSSVDDQYFLIGLYTF 60
|||||
QY 61 VSLIGFGNLLIIMALKRKNQKTTVFLIGNLAFSIDLVLVFCSPFTLTVSLDDQMF 120
|||||
Db 61 VSLIGFGNLLIIMALKRKNQKTTVFLIGNLAFSIDLVLVFCSPFTLTVSLDDQMF 120
|||||
QY 121 KWCHIMPFQOCVSVLSTILISIALVRYHMKRPSNNLTANHGFLATWTGLFAI 180
|||||
Db 121 KWCHIMPFQOCVSVLSTILISIALVRYHMKRPSNNLTANHGFLATWTGLFAI 180
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QY 181 CSPLPVHSLVELOEFGSALLSRVLCVSWPSDSRIRAFITSLILVOYILPLVCFVS 240
|||||
Db 181 CSPLPVHSLVELOEFGSALLSRVLCVSWPSDSRIRAFITSLILVOYILPLVCFVS 240
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Qy	Dy	Qy	Dy
24.1	HTSWCITRLKRRNNMMDKKROKKYSSSSRSRYEFTLLIIYFAVSWMDLPHFYVDEND 300	301	NLISNRHKKLVYCIICHLGMMSCCLNPIVLGFLNGLKADVSLTHCLHM 350
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RESULT 2
 US-09-771-956-10
 : Sequence 10, Application US/09771956
 : Patent No. US20010031474A1
 : GENERAL INFORMATION:
 : APPLICANT: Bennett, Michele
 : APPLICANT: Brobeck, Robbin
 : APPLICANT: Krause, James
 : TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
 : FILE REFERENCE: N2000.001
 : CURRENT APPLICATION NUMBER: US/09/771,956
 : CURRENT FILING DATE: 2001-01-29
 : NUMBER OF SEQ ID NOS: 31
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 10
 : LENGTH: 394
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA
 :S-09-771-956-10

	Query Match	96.8%: Score 1777: DB 10: Length 394:
	Best Local Similarity	99.4%: Pred. No. 9.4e-144:
	Matches 339: Conservative 1: Mismatches 1: Indels 0: Gaps 0:	
QY	1 MSFYSKQDYNNDELDEYYNKTATENNNTAATRNSDFEPMDDYKSSVDDLOYLGLGYTF 60	
Db	1 MSFYSKQDYNNDELDEYYNKTATENNNTAATRNSDFEPMDDYKSSVDDLOYLGLGYTF 60	
QY	61 VSLIGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDIILVLECSGFLLTSVLLDQMMFG 120	
Db	61 VSLIGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDIILVLECSGFLLTSVLLDQMMFG 120	
QY	121 KVMCHIMPELDCSVLSTVLTILISTAIYRHYHMKHPISNNLTANGYFLIAYVMTLGAII 180	
Db	121 KVMCHIMPELDCSVLSTVLTILISTAIYRHYHMKHPISNNLTANGYFLIAYVMTLGAII 180	
QY	181 CSPLPVFHSIVLELOETFGSALLSRYLCEVESPSDSYRIAFITISLLVYLIPVCLVYS 240	
Db	181 CSPLPVFHSIVLELOETFGSALLSRYLCEVESPSDSYRIAFITISLLVYLIPVCLVYS 240	
QY	241 HTSVICIRLKRNNNMKDKRDNKYRSSRSRSYVRLTILILVFAVSMPLHFLHVYTDEND 300	
Db	241 HTSVICIRLKRNNNMKDKRDNKYRSSRSRSYVRLTILILVFAVSMPLHFLHVYTDEND 300	
QY	301 NLISNRHFKLVYTCIHLIGMSSCLNPLLYGFLNNGICADL 341	
Db	301 NLISNRHFKLVYTCIHLIGMSSCLNPLLYGFLNNGICADL 341	

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RESULT 3
US-09-771-956-20
; Sequence 20, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000 001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31

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: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 20
: LENGTH: 341
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-20

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Query Match	94.98;	Score 1743;	DB 10;	Length 341;
Best Local Similarity	97.68;	Pred. No. 6.1e-141;		
Matches 332;	Conservative 4;	Mismatches 4;	Indels 0;	Gaps 0

Qy	11	MDLEDEXYNTLATENTTAATRSNDPWPMDYKSSVDDQOYFLIGLYTFVSLGFGNL	70
Db	1	MDLEQDPTNKTLATENTTAATRSNDPWPMDYKSSVDDQOYFLIGLYTFVSLGFGNL	60
Qy	71	LILALMKRNOKTTFVNLGNLAFSDILVVLFCSPPTLTSVLLDDOMFGKVMCHIMPL	130
Db	61	LILALMKRNOKTTFVNLGNLAFSDILVVLFCSPPTLTSVLLDDOMFGKVMCHIMPL	120
Qy	131	QCVSVLVTLLLSIAIYRYMIKHPISNNLTANHGFELATWTLGFAICSPLPVPHSL	190
Db	121	QCVSVLVTLLLSIAIYRYMIKHPISNNLTANHGFELATWTLGFAICSPLPVPHSL	180
Qy	191	VELOTFEGSALLSSRYLCVESWPSDYSRIAFTISLLVOYLPLVCLTVSHTSVCIRLKR	250
Db	181	VELOTFEGSALLSSRYLCVESWPSDYSRIAFTISLLVOYLPLVCLTVSHTSVCIRLKR	240
Qy	251	RNNMMDKKRDKYSSRSRSFYRLTLLIVFAVSWMPHLFHVHPDNNLISNRHFKL	310
Db	241	RNNMMDKKRDKYSSRSRSFYRLTLLIVFAVSWMPHLFHVHPDNNLISNRHFKL	300
Qy	311	YVCICHLIGMMSCLNPLVGFNLNGIKADLVSLICLHM	350
Db	301	YVCICHLIGMMSCLNPLVGFNLNGIKADLVSLICLHM	340

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1      RESULT 4
2      US-09-771-956-26
3      Sequence 26, Application US/09771956
4      Patent No. US2001003147A1
5      GENERAL INFORMATION:
6      APPLICANT: Bennett, Michele
7      APPLICANT: Brodbeck, Robbin
8      APPLICANT: Krause, James
9      TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
10     FILE REFERENCE: N2000.001
11     CURRENT APPLICATION NUMBER: US/09/771,956
12     CURRENT FILING DATE: 2001-01-29
13     NUMBER OF SEQ ID NOS: 31
14     SOFTWARE: PatentIn Ver. 3.1
15     SEQ ID NO 26
16     LENGTH: 341
17     TYPE: PRT
18     ORGANISM: Artificial Sequence
19     FEATURE:
20     OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERAN
21     US-09-771-956-26

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Query Match	92.5%	Score 1699:	DB 10:	Length 341:
Best Local Similarity	94.1%	Pred. No. 3.3e-137:		
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QY	11	MDLEDEYYNNTLAEENNTAATRNSDPVMWDYKSSVDLOQVFLGLGYFVSLGPMGL	70	
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :		
Db	1	MGSEIPDYNTKLASENNTVATRNSEGPVWDYKSSVDLOQVFLGLGYFVSLGPMGL	60	
QY	71	LILMAIMKRRKQKTVNFLIGNLAESDLIVYFCSPFTLSVLLDQMMGKVMCHIMPL	130	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	61	LILAAVMKRRKQKTVNFLIGNLAESDLIVYFCSPFTLSVLLDQMMGKVMCHIMPL	120	
QY	131	QCVSVLSTLILISAIYRYHNIKIPISNNLTAANGFYELIATVMTLGFACISPLPFSHL	190	

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Db 121 QCVTVLSTLILSLIAIVRYHMKHPVSNMLTANHGFLATVWTGLATCSPLPVFHSI 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 240
QY 251 RNMMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 310
Db 241 RNMMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 300
QY 311 VVICIHLGMMSCCLNPILYGFNLNGIKADVLISLHCLHM 350
Db 301 VVICIHLGMMSCCLNPILYGFNLNGIKADVLISLHCLHV 340

RESULT 5
US-09-771-956-21
; Sequence 21, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-21

Query Match          92.2%; Score 1693; DB 10; Length 383;
Best Local Similarity 97.6%; Pred. No. 1.2e-136;
Matches 333; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 MDLEDEYTKTLATENTNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLGEMGNL 70
Db 1 MDLEDDFYKTKLATENTNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLGEMGNL 60
QY 71 LILMALMKRRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMMEGKVMCHIMPEL 130
Db 61 LILMALMKRRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMMEGKVMCHIMPEL 120
QY 131 QCVSVLSTLILSLIAIVRYHMKHPISNNLTANHGFLATVWTGLATCSPLPVFHSI 190
Db 121 QCVSVLSTLILSLIAIVRYHMKHPISNNLTANHGFLATVWTGLATCSPLPVFHSI 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVCIRLKR 240
QY 251 RNMMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 310
Db 241 RNMMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNRHFKL 300
QY 311 VVICIHLGMMSCCLNPILYGFNLNGIKADVL 341
Db 301 VVICIHLGMMSCCLNPILYGFNLNGIQRDL 331

RESULT 6
US-09-771-956-23
; Sequence 23, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
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; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-23

Query Match          92.1%; Score 1691; DB 10; Length 352;
Best Local Similarity 92.4%; Pred. No. 1.6e-136;
Matches 318; Conservative 16; Mismatches 10; Indels 0; Gaps 0;
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```

QY 7 QDYNMDELDYNYKTLATENTNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTVFVSLG 66
Db 8 QDSSMEFKLEHFNKTFVETENNTAAARNAPAMEDYRGVDDIQYFLIGLYTVFVSLGF 67
QY 67 MGNLILMALMKRRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMMEGKVMCHI 126
Db 68 MGNLILMALMKRRKNOKTYNFFLIGNLAFSDIIVLFCSPFTLTSVLLDOMMEGKVMCHI 127
QY 127 MPFLQCVSVLSTLILSLIAIVRYHMKHPISNNLTANHGFLATVWTGLATCSPLPV 186
Db 128 MPFLQCVSVLSTLILSLIAIVRYHMKHPISNNLTANHGFLATVWTGLATCSPLPV 187
QY 187 FHSI VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVC 246
Db 188 FHSI VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVSHTSVC 247
QY 247 RLKRRNNMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNR 306
Db 248 RLKRRNNMDKMRDNKRRSSRSRSVFRILTLILVFAVSWMPHLFHVYTDNDNLISNR 307
QY 307 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADVLISLHCLHM 350
Db 308 HFKLVYICICHLGMMSCCLNPILYGFNLNGIKADVLISLHCLHM 351
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RESULT 7
US-09-771-956-13
; Sequence 13, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-956-13

Query Match          90.9%; Score 1668.5; DB 10; Length 455;
Best Local Similarity 73.2%; Pred. No. 1.8e-134;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
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QY 1 MSFYSKODYNMDELDYNYKTLATENTNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTF 60
Db 1 MSFYSKODYNMDELDYNYKTLATENTNTAATRNSDPFWDDYKSSVDDIQYFLIGLYTF 60
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OY 61 VSGGFMGNLLIMAKKKRQKQTKVNFIGNLAFSDIIVLECSPTTLTVLLDDMMFG 120
Db 61 VSLGFMGNLLIMAKKKRQKQTKVNFIGNLAFSDIIVLECSPTTLTVLLDDMMFG 120
OY 121 KVMCHIMPELOCVSVLSTLLISIAIVRYMHMKIPISNNLTANHGFFLIATVWTGFAI 180
Db 121 KVMCHIMPELOCVSVLSTLLISIAIVRYMHMKIPISNNLTANHGFFLIATVWTGFAI 180
OY 181 CSPLPVFHSIVLEOETFGSALLSRRYLCVBSWPSDRIAFVTSLLIYQIYIPLVCLTVS 240
Db 181 CSPLPVFHSIVLEOETFGSALLSRRYLCVBSWPSDRIAFVTSLLIYQIYIPLVCLTVS 240
OY 241 HTSVC---ILKRRNNMMOK----- 257
Db 241 HTSVCRTISGCLSKENKLENEEMINLTLPKSKSGQVAKLSGSHKWSYFIKKHRRYS 300
OY 258 -----RDNNKYR----- 264
Db 301 KKTACVLPAPERPQOENHSRLTPENFGSVSQQLSSSSKFLPGVPTCFETKPEPNSDVHEL 360
OY 265 -----SRSRSVFYRLLTILLVFAVSWMPHLFHVYVTDENDNLSNRHFKLYVCIC 315
Db 361 RKRRSVTRIKKRSRSVFYRLLTILLVFAVSWMPHLFHVYVTDENDNLSNRHFKLYVCIC 420
OY 316 HLLGMSQCLNPIIXGLFNGIKADIVSLHCLHM 350
Db 421 HLLGMSQCLNPIIXGLFNGIKADIVSLHCLHM 455

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RESULT 8
US-09-962-646-4
: Sequence 4, Application US/09962646
: Patent No. US20020103123A1
: GENERAL INFORMATION:
: APPLICANT: GERALD, CHRISTOPHE P.G.
: APPLICANT: WEINSHANK, RICHARD L.
: APPLICANT: WALKER, MARY M
: APPLICANT: BRANCHEK, THERESA
: TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, ANT
: TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECE
: FILE REFERENCE: 1795/4616BB/2A
: CURRENT APPLICATION NUMBER: US/09/962,646
: PRIOR FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: 09/200,673
: PRIOR FILING DATE: 1998-11-25
: PRIOR APPLICATION NUMBER: 08/566,096
: PRIOR FILING DATE: 1995-12-01
: PRIOR APPLICATION NUMBER: 08/349,025
: PRIOR FILING DATE: 1994-12-01
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 455
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-962-646-4

```

Query Match	90.9%;	Score 1668.5;	DB 10;	Length 455;
Best Local Similarity	73.2%;	Pred. No. 1.8e-134;		
Matches 333;	Conservative	6;	Mismatches 11;	Indels 105;
				Gaps 3;

QY	1	MSFSKODYNNDDLELDEYVYKNTTLATENNNTAATRSRSDPVMWDYKSSVDDLLQYFLIGLYTF	60
Db	1	MSFSKODYNNDDLELDEYVYKNTTLATENNNTAATRSRSDPVMWDYKSSVDDLLQYFLIGLYTF	60
QY	61	VSLIGPMGNLLILMALMKKRQKTTVNFIGNLAFSDILVYVFCSPPTLTLSVLLDDMG	120
Db	61	VSLIGPMGNLLILMALMKKRQKTTVNFIGNLAFSDILVYVFCSPPTLTLSVLLDDMG	120
QY	121	KVMCHIMPLQCVSVLSTLILSIAIVRHHMKHPSNNLTVANHGFLATVWTIGFAL	180
Db	121	KVMCHIMPLQCVSVLSTLILSIAIVRHHMKHPSNNLTVANHGFLATVWTIGFAL	180

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QY      181  CSPLPVHSLVLEQETBSALLSRVLCVSWBPDSTRIAFTISLLVOYLPLRYCLTVS  240
Db      181  CSPLPVHSLVLEQETBSALLSRVLCVSWBPDSTRIAFTISLLVOYLPLRYCLTVS  240
QY      241  HTSVC---IRLKRNNMMDK-----257
          |||||      | : : :
Db      241  HTSVCRSISCGLSKNENLENEINLTLPKSKSGPQVYLKSGHKWSYFIIKHHRRYS  300
QY      258  -----RDNRKYR-----264
          : : : |
Db      301  KKTACVLPAPEPSPQENNSRIILPENFGSVRSQSSSKFTLPVPTCFEIKPEENSDVHEL  360
QY      265  -----SSRSRSVYFRLTILILVFAVSMPLHLFHVYTFDNDNLISNRHFKLYVCIC  315
          |||||
Db      361  RYKRSVTRIKKRKRSVYFRLTILILVFAVSMPLHLFHVYTFDNDNLISNRHFKLYVCIC  420
QY      316  HILGMSCLNPILYGLPLNNIKRDLVSLIHCLHM  350
          |||||
Db      421  HILGMSCLNPILYGLPLNNIKRDLVSLIHCLHM  455

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RESULT 9
US-09-771-956-30
; Sequence 30, Application US/09771956
; Patent No. US2001003147A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Cercopithecus aethiops
US-09-771-956-30

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Query Match 90.7%; Score 1665.5; DB 10; Length 455;
Best Local Similarity 73.0%; Pred. No. 3.2e-134;
Matches 332; Conservative 7; Mismatches 11; Indels 105; Gaps 3

Qy	1	MSISKODYNMDELDEYXNKTATENNATRRSDPVMDDXSSVDDLOQYLIGLYTF	60
Db	1	MSFSKODYNMDELDEYXNKTATENNATRRSDPVMDDXSSVDDLOQYLIGLYTF	60
Qy	61	VSLIGFPMNLILMALMKRKQKTTVNFELIGNLAFSDILVLPFCSPTLTVSLDDQMMFG	120
Db	61	VSLIGFPMNLILMALMKRKQKTTVNFELIGNLAFSDILVLPFCSPTLTVSLDDQMMFG	120
Qy	121	KVMCHIMPELQCVSVLSTLLISIAIVRYMHKIPISNNLTANHGYELIATVWTLGFAI	180
Db	121	KVMCHIMPELQCVSVLSTLLISIAIVRYMHKIPISNNLTANHGYELIATVWTLGFAI	180
Qy	181	CSPLPVFHSLVELOETFGSALLSSRYLCLVCSWBPDSRIATFISLLVOYLPLVCLTVS	240
Db	181	CSPLPVFHSLVELOETFGSALLSSRYLCLVCSWBPDSRIATFISLLVOYLPLVCLTVS	240
Qy	241	HTSWC---IRLKRRNNMDC-----	257
Db	241	HTSWC---IRLKRRNNMDC-----	257
Qy	258	-----MRDNKYR-----	264
Db	301	KKTACVLPAPERPQDHNHSLRLLPFGSVPYSQSLSSSSKFLIPGYTCPEIRPENSDVHEL	360
Qy	265	-----SSRSBSVFYRLTILILVAVSWMPLHLEHVVTDFENDNLISNRHFKLYVCIC	315
Db	361	RKRSVTRIKRKSBSVFYRLTILILVAVSWMPLHLEHVVTDFENDNLISNRHFKLYVCIC	420

[illegible]

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-25

Query Match      89.2%; Score 1637; DB 10; Length 395;
Best Local Similarity 92.8%; Pred. No. 7,2e-132;
Matches 308; Conservative 15; Mismatches 9; Indels 0; Gaps 0.

OY 7 GQYNNMDELDEYYNKTLATENNMTAATRNSDPPYWDYKSSVDDLOYFLGLTVPYSLGFG 66
   ||:::|:|:||||| ||||| ||: || |::| ||||| ||||| ||||| |||||
DB 8 QSSSEFEKLEEHFNKTEVENNTAARNAAPFAMEDYKRSVDDLOYFLGLTVPYSLGFG 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 67 MGNLIILAMLMKRRNOKTTVNFIQNLAFSDILVYLFCSPTLTSVLLDQMGKWMCHI 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 68 MGNLIILAMVMKRRNOKTTVNFIQNLAFSDILVYLFCSPTLTSVLLDQMGKWMCHI 127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 127 MPFLQCVSLVSTLLISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFALCSPLPV 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 128 MPFLQCVSLVSTLLISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFALCSPLPV 187
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 187 FHSIVLEOTFESSALLSRYLCVESWPSDYSRIAFITISLLVOYLIPVCLVSHTSVCI 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 FHSIVLEKTFESSALLSRYLCVESWPSDYSRIAFITISLLVOYLIPVCLVSHTSVCI 247
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 247 RLRKRRNNMDKRRDNKRYRSRSRSYFRLTILILVFAVSMPLHLFHVYTDENDLISNR 306
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 248 RLRKRRNNMDKTRDSKYSRSRSYFRLTILILVFAVSMPLHLFHVYTDENDLISNR 307
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 307 HEKLVYCICHLGLGMMSCCLNPILYGFLLNGIK 338
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 308 HEKLVYCICHLGLGMMSCCLNPILYGFLLNGIK 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-771-956-9
; Sequence 9, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y5/Y1 CHIMERA
US-09-771-956-9

Query Match      87.7%; Score 1609.5; DB 10; Length 499;
Best Local Similarity 72.2%; Pred. No. 2e-129;
Matches 322; Conservative 7; Mismatches 12; Indels 105; Gaps 3;

OY 1 MSFYSKODYNNMDELDEYYNKTLATENNMTAATRNSDPPYWDYKSSVDDLOYFLGLTYTF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MSFYSKODYNNMDELDEYYNKTLATENNMTAATRNSDPPYWDYKSSVDDLOYFLGLTYTF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 VSLGFMGNLILMALMKRRNOKTTVNFIQNLAFSDILVYLFCSPTLTSVLLDQMGK 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 VSLGFMGNLILMALMKRRNOKTTVNFIQNLAFSDILVYLFCSPTLTSVLLDQMGK 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 KVMCHIMPFLOCVSLVSTLLISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFAL 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 KVMCHIMPFLOCVSLVSTLLISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGFAL 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 CSPLEVFHSIVLEOTFESSALLSRYLCVESWPSDYSRIAFITISLLVOYLIPVCLTVS 240

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Db 181 CSPLPEFHSVLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVS 240
QY 241 HTSVC-----IRLKRNNMMDK----- 257
Db 241 HTSVCRSISCSLSKNENLEENEMINTLPHSKSGPOVKLSGSHKWSYFIKKHRRYS 300
QY 258 -----MRDNKYR----- 264
Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQLSSSSKFIDCVPTCFELKPENSDVHEL 360
QY 265 -----SSRSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCIC 315
Db 361 RVKRSVTRIKKRSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCIC 420
QY 316 HLLGMSCLNPILYGFNLNGIKADL 341
Db 421 HLLGMSCLNPILYGFNLNGIQDRL 446

RESULT 13
US-09-962-646-2
; Sequence 2, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L.
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHER, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; FILE REFERENCE: 1795/46166BA
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US/09/962, 646
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566, 096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349, 025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Rattus No. US20020103123A1veglicus
US-09-962-646-2

Query Match 83.7%; Score 1536; DB 10; Length 456;
Best Local Similarity 67.9%; Pred. No. 3.1e-123;
Matches 304; Conservative 21; Mismatches 19; Indels 104; Gaps 3;
QY 7 ODYWMDELDEYUKTLATENNATRSDEPVDYKSSVDDLOVFLIGLYTVSLLGF 66
Db 8 ODSSMERLEHFNKTYTENNATAARNAAPAMEDYRGSDVDDLOVFLIGLYTVSLLGF 67
QY 67 MGNLLILMALKKRNOKTYVFLIGNLAFSDILVLFCSPTLTSVLLDOMFGKVMCHI 126
Db 68 MGNLLILMAVKKRNOKTYVFLIGNLAFSDILVLFCSPTLTSVLLDOMFGKVMCHI 127
QY 127 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 186
Db 128 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 187
QY 187 FHSVLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVSHTSVC- 245
Db 188 FHSVLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVSHTSVC- 247
QY 246 ---IRLKRNNMMDK-----MRDNKYRS----- 266
Db 248 SISGSLSHKERNLEENEMINTLPHSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACV 307
QY 267 ----- 266

Db 308 LPAPAGPSQGNHVAENPASVRSQLSPPSKVIRGVPICFEVKEPDESSDAHEMRKRSIT 367
QY 267 ---RSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCICHLGMS 322
Db 368 RIKKRSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCICHLGMS 427
QY 323 CCLNPILYGFNLNGIKADVLSLHCLHM 350
Db 428 CCLNPILYGFNLNGIKADVLSLHCLHM 455

RESULT 14
US-09-771-956-24
; Sequence 24, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000-001
; CURRENT APPLICATION NUMBER: US/09/771, 956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Y1/Y5 CHIMERA
US-09-771-956-24

Query Match 80.7%; Score 1482; DB 10; Length 499;
Best Local Similarity 67.4%; Pred. No. 1.3e-118;
Matches 294; Conservative 20; Mismatches 18; Indels 104; Gaps 3;
QY 7 ODYWMDELDEYUKTLATENNATRSDEPVDYKSSVDDLOVFLIGLYTVSLLGF 66
Db 8 ODSSMERLEHFNKTYTENNATAARNAAPAMEDYRGSDVDDLOVFLIGLYTVSLLGF 67
QY 67 MGNLLILMALKKRNOKTYVFLIGNLAFSDILVLFCSPTLTSVLLDOMFGKVMCHI 126
Db 68 MGNLLILMAVKKRNOKTYVFLIGNLAFSDILVLFCSPTLTSVLLDOMFGKVMCHI 127
QY 127 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 186
Db 128 MPFLQCVSVLSTLILISIAIVRYHMIKHPISNNLTANHGFLATYWTGFAICSPLPV 187
QY 187 FHSVLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVSHTSVC- 245
Db 188 FHSVLVELOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVOYILPLVCLTVSHTSVC- 247
QY 246 ---IRLKRNNMMDK-----MRDNKYRS----- 266
Db 248 SISGSLSHKERNLEENEMINTLPHSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACV 307
QY 267 ----- 266
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QY 267 ---RSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCICHLGMS 322
Db 368 RIKKRSRSVFRLTILILVFAVSWMPHLFHVVDNFNDNLISNRHFKLVYCICHLGMS 427
QY 323 CCLNPILYGFNLNGIK 338
Db 428 CCLNPILYGFNLNGIK 443
RESULT 15
US-09-771-956-22

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:08:44 : Search time 14 Seconds
(without alignments)
735.573 Million cell updates/sec

Title: US-09-771-956-6

Perfect score: 1836
Sequence: 1 MSFYSKQDYNMDELDELYNN.....GFLNNGIKADLVSLHCLHM 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1668.5	90.9	455	1	US-08-349-025-4
2	1668.5	90.9	455	2	US-08-566-096A-4
3	1668.5	90.9	455	2	US-08-668-650B-4
4	1668.5	90.9	455	4	US-09-200-673-4
5	1668.5	90.9	456	5	PCT-US95-15646-4
6	1616.5	88.0	456	2	US-08-668-650B-14
7	1613.5	87.9	445	2	US-08-630-118A-6
8	1613.5	87.9	445	2	US-08-838-399-6
9	1613.5	87.9	445	2	US-09-003-199-21
10	1613.5	87.9	445	4	US-09-235-839-6
11	1610.5	87.7	445	4	US-09-327-035-6
12	1610.5	87.7	445	4	US-09-040-958-2
13	1610.5	87.7	445	4	US-09-040-958-4
14	1549.5	84.4	456	2	US-09-003-199-2
15	1536	83.7	456	1	US-08-349-025-2
16	1536	83.7	456	2	US-08-566-096A-2
17	1536	83.7	456	2	US-08-668-650B-2
18	1536	83.7	456	4	US-09-200-673-2
19	1536	83.7	456	5	PCT-US95-15646-2
20	1526	83.1	445	2	US-08-630-118A-4
21	1526	83.1	445	2	US-08-838-399-4
22	1526	83.1	445	2	US-09-003-199-23
23	1526	83.1	445	4	US-09-235-839-4
24	1526	83.1	445	4	US-09-327-035-4
25	1519	82.7	445	2	US-08-630-118A-2
26	1519	82.7	445	2	US-08-838-399-2
27	1519	82.7	445	4	US-09-235-839-2

28	1519	82.7	445	4	US-09-327-035-2	Sequence 2, App11
29	1025.5	55.9	334	2	US-08-566-096A-6	Sequence 6, App11
30	1025.5	55.9	334	2	US-08-668-650B-6	Sequence 6, App11
31	1025.5	55.9	334	4	US-09-200-673-6	Sequence 6, App11
32	1025.5	55.9	334	5	PCT-US95-15646-6	Sequence 6, App11
33	644	35.1	383	3	US-09-045-186-2	Sequence 2, App11
34	644	35.1	384	1	US-08-232-144-4	Sequence 4, App11
35	644	35.1	384	4	US-08-555-268A-15	Sequence 15, App1
36	644	35.1	384	5	PCT-US93-05039-3	Sequence 3, App11
37	638	34.7	384	4	US-09-200-673-15	Sequence 15, App1
38	633.5	34.5	382	1	US-08-415-818-7	Sequence 7, App11
39	633.5	34.5	382	2	US-08-894-236-7	Sequence 7, App11
40	633.5	34.5	382	2	US-08-555-268A-13	Sequence 13, App1
41	633.5	34.5	382	2	US-08-555-268A-14	Sequence 14, App1
42	633.5	34.5	382	5	PCT-US96-01444-7	Sequence 7, App11
43	620	33.8	411	5	US-08-817-869-3	Sequence 3, App11
44	620	33.8	411	5	PCT-US95-14377-3	Sequence 3, App11
45	552.5	30.1	371	1	US-08-415-818-6	Sequence 6, App11

ALIGNMENTS

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RESULT 1
US-08-349-025-4
: Sequence 4, Application US/08349025
: Patent No. 5602024
: GENERAL INFORMATION:
: APPLICANT: Gerald, Christophe P.G.
: APPLICANT: Walker, Mary W.
: APPLICANT: Branchek, Theresa
: APPLICANT: Weinschank, Richard L.
: TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
: TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YX RECEPTOR (Y5) AND USES THEREOF
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/349,025
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 1795/46166
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: TELEX: 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 455 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-349-025-4

Query Match 90.9% Score 1668.5; DB 1; Length 455;
Best local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
1 MSFYSKQDYNMDELDELYNNKTLATENRATRNDFPPWVDYKSSVDLQYFLIGLYTF 60
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Db 1 MSFYSKDYNNMDELDEYYNKTATENNATATRNDFPVDYKSSVDDLYFLIGLYTF 60
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Db 61 VSLGFMGNLLILMALMKRRKQKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDQMMEG 120
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYMHKIPISNNLTANNGYFLIATVWTIGFAI 180
Db 121 KVMCHIMPELOCVSVLSTLLISAIYRYMHKIPISNNLTANNGYFLIATVWTIGFAI 180
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVS 240
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVS 240
QY 241 HTSVC---ITLKRNNMDK----- 257
Db 241 HTSVCRSISGCLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
QY 258 -----MRDNKYY----- 264
Db 301 KKTACVLPAPRRPOENHSRLPENFGSVRSQSSSKFICGPTCFEIKPEENSDVHEL 360
QY 265 -----SSRSVFEYRTILILVFAVSWMPHLFHVYTDNDNLISNHFPLYVCIC 315
Db 361 RVKRSVTRIKKRSRSVEFRTILILVFAVSWMPHLFHVYTDNDNLISNHFPLYVCIC 420
QY 316 HLLGMMSCCLNPILYGFLNNGIKADIVSLIHCLHM 350
Db 421 HLLGMMSCCLNPILYGFLNNGIKADIVSLIHCLHM 455

RESULT 2
US-08-566-096A-4
Sequence 4, Application US/08566096A
Patent No. 5968819
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR,
TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC
TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YX RECEPTOR (Y5) AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,096A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-566-096A-4
Query Match 90.9%; Score 1668.5; DB 2; Length 455;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 1 MSFYSKDYNNMDELDEYYNKTATENNATATRNDFPVDYKSSVDDLYFLIGLYTF 60
Db 1 MSFYSKDYNNMDELDEYYNKTATENNATATRNDFPVDYKSSVDDLYFLIGLYTF 60
QY 61 VSLGFMGNLLILMALMKRRKQKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDQMMEG 120
Db 61 VSLGFMGNLLILMALMKRRKQKTTVNFILGNLAFSDILVYLFCSPTLTYSVLDQMMEG 120
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYMHKIPISNNLTANNGYFLIATVWTIGFAI 180
Db 121 KVMCHIMPELOCVSVLSTLLISAIYRYMHKIPISNNLTANNGYFLIATVWTIGFAI 180
QY 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVS 240
Db 181 CSPLPVFHSLVELOETFGSALLSRYLCVESWPSDSYRIAFITISLLVOYLPLVCLTVS 240
QY 241 HTSVC---ITLKRNNMDK----- 257
Db 241 HTSVCRSISGCLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
QY 258 -----MRDNKYY----- 264
Db 301 KKTACVLPAPRRPOENHSRLPENFGSVRSQSSSKFICGPTCFEIKPEENSDVHEL 360
QY 265 -----SSRSVFEYRTILILVFAVSWMPHLFHVYTDNDNLISNHFPLYVCIC 315
Db 361 RVKRSVTRIKKRSRSVEFRTILILVFAVSWMPHLFHVYTDNDNLISNHFPLYVCIC 420
QY 316 HLLGMMSCCLNPILYGFLNNGIKADIVSLIHCLHM 350
Db 421 HLLGMMSCCLNPILYGFLNNGIKADIVSLIHCLHM 455
RESULT 3
US-08-668-650B-4
Sequence 4, Application US/08668650B
Patent No. 5989920
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,
TITLE OF INVENTION: Compounds Useful in Such Methods, and DNA Encoding a
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YX Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,650B
FILING DATE: 04-JUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166C

```

TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 455 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-668-6508-4

Query Match      90.9%; Score 1668.5; DB 2; Length 455;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

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DB 1 MSFYSKODYNDLEDEYNNKTATENTNTATRNSDPFVMDYKSSVDDLYFLIGLYTF 60
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DB 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVLFCSPTFLTSVLLDQWFG 120
QY 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
DB 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
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DB 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
QY 181 CSPLPVFHSVLEOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSVLEOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVC---IRLKRNNMMDK----- 257
DB 241 HTSVCRSISGCLSKENLEENEMINLTHPSKSGQVYKLSGSHKMSYFIKKHRRYS 300
QY 258 -----MRDNKYR----- 264
DB 301 KKTACVLPAPERPSOENHSRLPENFGSVRSQSSSKFIPGVTCEFIKEPENSVDHEL 360
QY 265 -----SSRSRSVFYRLTILILVFAVSWMPHLPHVYTDENDNLISNHFPLYVCIC 315
DB 361 RVKRSVTRIKRKSRSVFRLTILILVFAVSWMPHLPHVYTDENDNLISNHFPLYVCIC 420
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DB 421 HLLGMMSCLNPILYGLFNLNGIKADLVSLIHCLHM 455

RESULT 4
US-09-200-673-4
: Sequence 4, Application US/09200673A
: Patent No. 6316203
: GENERAL INFORMATION:
: APPLICANT: Gerald, Christophe P.G.
: APPLICANT: Weisshank, Richard L.
: APPLICANT: Walker, Mary W.
: APPLICANT: Branchek, Theresa
: TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
: TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic
: TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide Y Receptor (Y5)
: FILE REFERENCE: 46166-B2/JPM
: CURRENT APPLICATION NUMBER: US/09/200,673A
: EARLIER FILING DATE: 1998-11-25
: EARLIER APPLICATION NUMBER: 08/566,096
: EARLIER FILING DATE: 1995-12-01
: EARLIER APPLICATION NUMBER: 08/349,025
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 455
: TYPE: PRT
: ORGANISM: Homo sapiens

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US-09-200-673-4
Query Match      90.9%; Score 1668.5; DB 4; Length 455;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 1 MSFYSKODYNDLEDEYNNKTATENTNTATRNSDPFVMDYKSSVDDLYFLIGLYTF 60
DB 1 MSFYSKODYNDLEDEYNNKTATENTNTATRNSDPFVMDYKSSVDDLYFLIGLYTF 60
QY 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVLFCSPTFLTSVLLDQWFG 120
DB 61 VSLGFMGNLLILALMKRRNQKTTVNFLIGNLAFSDILVLFCSPTFLTSVLLDQWFG 120
QY 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
DB 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
QY 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
DB 121 KVMCHIMPFLOCVSVLSTLLISAIYRYMHKHPISNNLTANHGFLLIATVWTGLFAI 180
QY 181 CSPLPVFHSVLEOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSVLEOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVC---IRLKRNNMMDK----- 257
DB 241 HTSVCRSISGCLSKENLEENEMINLTHPSKSGQVYKLSGSHKMSYFIKKHRRYS 300
QY 258 -----MRDNKYR----- 264
DB 301 KKTACVLPAPERPSOENHSRLPENFGSVRSQSSSKFIPGVTCEFIKEPENSVDHEL 360
QY 265 -----SSRSRSVFYRLTILILVFAVSWMPHLPHVYTDENDNLISNHFPLYVCIC 315
DB 361 RVKRSVTRIKRKSRSVFRLTILILVFAVSWMPHLPHVYTDENDNLISNHFPLYVCIC 420
QY 316 HLLGMMSCLNPILYGLFNLNGIKADLVSLIHCLHM 350
DB 421 HLLGMMSCLNPILYGLFNLNGIKADLVSLIHCLHM 455

RESULT 5
PCT-US95-15646-4
: Sequence 4, Application PC/TUS9515646
: GENERAL INFORMATION:
: APPLICANT: Synaptic Pharmaceutical Corporation
: TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS
: TITLE OF INVENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATY
: TITLE OF INVENTION: Y/PEPTIDE Y RECEPTOR (Y5) AND USES THEREOF
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/15646
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 1795/46166-A-PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:

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LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15646-4

Query Match 90.9%; Score 1668.5; DB 5; Length 456;
Best Local Similarity 73.2%; Pred. No. 8.8e-135;
Matches 333; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 1 MSFYSKODYNNDELDEYYNKTATENNATATRNSDPFVMDYKSSVDDLOYLFLGLYTF 60
DB 1 MSFYSKODYNNDELDEYYNKTATENNATATRNSDPFVMDYKSSVDDLOYLFLGLYTF 60
QY 61 VSLGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLLDQMMFG 120
DB 61 VSLGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLLDQMMFG 120
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKHPISNNLTANHGYFLIATVMTLGFAT 180
DB 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKHPISNNLTANHGYFLIATVMTLGFAT 180
QY 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240
DB 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240
QY 241 HTSVC---IRLKRNNMMDK----- 257
DB 241 HTSVCRSISGLSNKENLEENEMINLTLPFSKSGPQVKLSGHKMSYSFIKKHRRYS 300
QY 258 -----MRDNKRY----- 264
DB 301 KKTACVLPAPARPOENHSRLPENFGSVRSQSSSKFTIGVPTCFEIKPEENSDVHEL 360
QY 265 -----SRSRSRYFRLTILILVEFVSWMPHLFHVVTDFDNDLNSNHFRLVYCIC 315
DB 361 RVKRSVTRIKRKRSSVFRILITILVEFVSWMPHLFHVVTDFDNDLNSNHFRLVYCIC 420
QY 316 HLLGMSCCLNPILYGLFNLNGIKADVLSTLHCLHM 350
DB 421 HLLGMSCCLNPILYGLFNLNGIKADVLSTLHCLHM 455

RESULT 6
US-08-668-650B-14
Sequence 14, Application US/08668650B
Patent No. 5983920
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Baker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Welinshank, Richard L.
TITLE OF INVENTION: Methods of Modifying Feeding Behavior,
TITLE OF INVENTION: Compounds useful in such Methods, And DNA Encoding a
TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide Y Receptor
NUMBER OF INVENTION: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,650B
FILING DATE: 04-JUN-1996
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-650B-14

Query Match 88.0%; Score 1616.5; DB 2; Length 456;
Best Local Similarity 71.6%; Pred. No. 2.4e-130;
Matches 326; Conservative 8; Mismatches 16; Indels 105; Gaps 3;

QY 1 MSFYSKODYNNDELDEYYNKTATENNATATRNSDPFVMDYKSSVDDLOYLFLGLYTF 60
DB 1 MSFYSKODYNNDELDEYYNKTATENNATATRNSDPFVMDYKSSVDDLOYLFLGLYTF 60
QY 61 VSLGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLLDQMMFG 120
DB 61 VSLGFMGNLLILMALMKRRNOKTTVNFLLIGNLAFSDILVYLFCSPTLTSLVLLDQMMFG 120
QY 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKHPISNNLTANHGYFLIATVMTLGFAT 180
DB 121 KVMCHIMPELOCVSVLSTLLISAIYRYHMKHPISNNLTANHGYFLIATVMTLGFAT 180
QY 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240
DB 181 CSPLPVEHSLVELOETFGSALLSSRYLCVESMPSDSYRIAFETISLLVQYILPLVCLTVS 240
QY 241 HTSVC-----IRLKR----- 251
DB 241 HTSVCRSISGLSNKENLEENEMINLTLPFSKSGPQVKLSGHKMSYSFIKKHRRYS 300
QY 252 -----NNMDKM 258
DB 301 KKTACVLPAPARPOENHSRLPENFGSVRSQSSSKFTIGVPTCFEIKPEENSDVHDM 360
QY 259 RDNK---YRSRSRYFRLTILILVEFVSWMPHLFHVVTDFDNDLNSNHFRLVYCIC 315
DB 361 RVKRSIMIKRKRSSVFRILITILVEFVSWMPHLFHVVTDFDNDLNSNHFRLVYCIC 420
QY 316 HLLGMSCCLNPILYGLFNLNGIKADVLSTLHCLHM 350
DB 421 HLLGMSCCLNPILYGLFNLNGIKADVLSTLHCLHM 455

RESULT 7
US-08-630-118A-6
Sequence 6, Application US/08630118A
Patent No. 5919901
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
APPLICANT: McCalieb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
TITLE OF INVENTION: Sequences
NUMBER OF INVENTION: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McDonnell Boelnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,118A
FILING DATE: April 8, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-118A-6
```

```

Query Match      87.9%; Score 1613.5; DB 2; Length 445;
Best Local Similarity 72.6%; Pred. No. 4,2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
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QY 11 MDLEDEYKTKLTATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
D 1 MDLEDEYKTKLTATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60
QY 71 LLMALMKKRNQKTTVNFLLGNLAFSDILVVLFCSPPTLTSVLLDDQMFQKVMCHIMPFL 130
D 61 LLMALMKKRNQKTTVNFLLGNLAFSDILVVLFCSPPTLTSVLLDDQMFQKVMCHIMPFL 120
QY 131 QCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 190
D 121 QCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 180
QY 191 VELOETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVC-----I 246
D 181 VELOETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVC-----I 240
QY 247 RLKRRNNMMK-----S 257
D 241 GLSKNEKRLLENEMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRRSKKTACVLPAP 300
QY 258 ---MRDNKYR-----S 265
D 301 ERPSQENHSRLPENFGSVASQSSSKFTIPGVPTCEIKPEENSDVHELRYKRSVTRIK 360
QY 266 SRSRSVYFRLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLYYCICHLGMMSCCL 325
D 361 KRSRSVYFRLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLYYCICHLGMMSCCL 420
QY 326 NPILYGLNNGIKADVSLIHCLHM 350
D 421 NPILYGLNNGIKADVSLIHCLHM 445

RESULT 8
US-08-638-399-6
; Sequence 6, Application US/0838399
; Patent No. 5965392
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: Mccaled Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; TITLE OF INVENTION: Sequences
; NUMBER OF SEQUENCES: 8
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,399
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-399-6
```

```

Query Match      87.9%; Score 1613.5; DB 2; Length 445;
Best Local Similarity 72.6%; Pred. No. 4,2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
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```

QY 11 MDLEDEYKTKLTATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
D 1 MDLEDEYKTKLTATENNATATNSDPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60
QY 71 LLMALMKKRNQKTTVNFLLGNLAFSDILVVLFCSPPTLTSVLLDDQMFQKVMCHIMPFL 130
D 61 LLMALMKKRNQKTTVNFLLGNLAFSDILVVLFCSPPTLTSVLLDDQMFQKVMCHIMPFL 120
QY 131 QCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 190
D 121 QCVSVLSTLLISIAIVRYHMKHPISNNLTANHGYFLATVWTGFAICSPLPVHSL 180
QY 191 VELOETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVC-----I 246
D 181 VELOETFGSALLSSRYLCVSWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVC-----I 240
QY 247 RLKRRNNMMK-----S 257
D 241 GLSKNEKRLLENEMINTLHPSSKSGPOVKLSGSHKWSYFIKKHRRRSKKTACVLPAP 300
QY 258 ---MRDNKYR-----S 265
D 301 ERPSQENHSRLPENFGSVASQSSSKFTIPGVPTCEIKPEENSDVHELRYKRSVTRIK 360
QY 266 SRSRSVYFRLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLYYCICHLGMMSCCL 325
D 361 KRSRSVYFRLTILVFAVSMPLHLFHVYTDNFNDNISNRHFKLYYCICHLGMMSCCL 420
QY 326 NPILYGLNNGIKADVSLIHCLHM 350
D 421 NPILYGLNNGIKADVSLIHCLHM 445

RESULT 9
US-09-003-199-21
; Sequence 21, Application US/09003199
; Patent No. 5985616
; GENERAL INFORMATION:
```

APPLICANT: Parker, Eric M
APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: NJ
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,199
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thampoe, Immac J
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN0775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)298-5061
TELEFAX: (908)298-5388
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-199-21

Query Match 87.9%; Score 1613.5; DB 2; Length 445;
Best Local Similarity 72.6%; Pred. No. 4.2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 11 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 70
Db 1 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 60
QY 71 LILALMKRRNQKTTVNFLLGNLAFSDILVVLFCSPFTLTSVLLDQWFGKVMCHIMFPL 130
Db 61 LILALMKRRNQKTTVNFLLGNLAFSDILVVLFCSPFTLTSVLLDQWFGKVMCHIMFPL 120
QY 131 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFALCSPLPVPHSL 190
Db 121 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFALCSPLPVPHSL 180
QY 191 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVC---I 246
Db 181 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240
QY 247 RLKRRNNMMDK----- 257
Db 241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKMSYFIKKHRRRYSKTACVLPAP 300
QY 258 ---MRDNKYR-----S 265
Db 301 ERPSQENHSRLPENFGSVRSQSSSKFLPGVPTCFEIKPEENSDVHELKRSVTRIK 360
QY 266 SRSQSVYRLTLLVFAVSMPLHLFHVYTDENDNLISNHEKLYVCICHLGMSGCL 325
Db 361 KRSSSVYRLTLLVFAVSMPLHLFHVYTDENDNLISNHEKLYVCICHLGMSGCL 420
QY 326 NPILYGLNNGIKADLVSLIHCLHM 350
Db 421 NPILYGLNNGIKADLVSLIHCLHM 445

RESULT 10
US-09-235-839-6
Sequence 6, Application US/09235839
Patent No. 6207799
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
APPLICANT: McCalcd Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,839
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,118
FILING DATE: April 8, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-235-839-6

Query Match 87.9%; Score 1613.5; DB 4; Length 445;
Best Local Similarity 72.6%; Pred. No. 4.2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;
QY 11 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 70
Db 1 MDLEDEYNTLTATENTTAATRNSDPFVMDYKSSVDDLOFLIGLYTFVSLGFMGNL 60
QY 71 LILALMKRRNQKTTVNFLLGNLAFSDILVVLFCSPFTLTSVLLDQWFGKVMCHIMFPL 130
Db 61 LILALMKRRNQKTTVNFLLGNLAFSDILVVLFCSPFTLTSVLLDQWFGKVMCHIMFPL 120
QY 131 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFALCSPLPVPHSL 190
Db 121 QCVSVLVSTLLISIAIVRYHMKHPISNNLTANHGFLATVWTLGFALCSPLPVPHSL 180
QY 191 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVC---I 246
Db 181 VELOETFGSALLSRVLCVESMPDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240
QY 247 RLKRRNNMMDK----- 257
Db 241 GLSNKENRLEENEMINLTLPSSKSGPOVKLSGSHKMSYFIKKHRRRYSKTACVLPAP 300
QY 258 ---MRDNKYR-----S 265

Db 301 ERPSQEHSHILPENFGSVRSQSSSKFTPGVPTCEIKPEENSDVHELVRKRVTRIK 360
QY 266 SRSRSVFRLLTLLILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCIHLLGMSSCCL 325
|||||
Db 361 KRSRSVFRLLTLLILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCIHLLGMSSCCL 420
QY 326 NPILYGFLLNGIKADLVSLIHCLHM 350
|||||
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 11
US-09-327-035-6
; Sequence 6, Application US/09327035
; Patent No. 6368824
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; McCaleb Ph.D., Michael L.
; Bloomquist Ph.D., Brian T.
; Flores-Riveros Ph.D., Jaime R.
; Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/327,035
; FILING DATE: 07-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,399
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-327-035-6

Query Match 87.9%; Score 1613.5; DB 4; Length 445;
Best Local Similarity 72.6%; Pred. No. 4.2e-130;
Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps 3;

QY 11 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
|||||
Db 1 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60
QY 71 L1MALMKRRNOKTYVNFILGNLAFSDDLVLVLFCSPTLTSVLLDDQMGKVMCHIMPEL 130
|||||
Db 61 L1MALMKRRNOKTYVNFILGNLAFSDDLVLVLFCSPTLTSVLLDDQMGKVMCHIMPEL 120
QY 131 QCVSVLVSTLILSLIAIVRYHMKRPIISNNLTANHGFFLIATYWTGFAICSPLPVPHSL 190
|||||

Db 121 QCVSVLVSTLILSLIAIVRYHMKRPIISNNLTANHGFFLIATYWTGFAICSPLPVPHSL 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITSLILVOYLPLVCLVTSHTSVSC----I 246
|||||
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITSLILVOYLPLVCLVTSHTSVSCISIC 240
QY 247 RLKRRNNMMDK----- 257
| : | : :
Db 241 GLSNKENRELEENEMINLTLPSSKSGPQVYKLSGSHKWSYFIKKHRRYSKTKACVLPAP 300
QY 258 ---MDKKYR-----S 265
| : | : |
Db 301 ERPSQEHSHILPENFGSVRSQSSSKFTPGVPTCEIKPEENSDVHELVRKRVTRIK 360
QY 266 SRSRSVFRLLTLLILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCIHLLGMSSCCL 325
|||||
Db 361 KRSRSVFRLLTLLILVFAVSMPLHLFHVYTDNDNLISNRHFKLVYCIHLLGMSSCCL 420
QY 326 NPILYGFLLNGIKADLVSLIHCLHM 350
|||||
Db 421 NPILYGFLLNGIKADLVSLIHCLHM 445

RESULT 12
US-09-040-958-2
; Sequence 2, Application US/09040958
; Patent No. 6242251
; GENERAL INFORMATION:
; APPLICANT: Baez, Melvyn
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y5 RECEPTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,958
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-11350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-040-958-2

Query Match 87.7%; Score 1610.5; DB 4; Length 445;
Best Local Similarity 72.4%; Pred. No. 7.5e-130;
Matches 322; Conservative 7; Mismatches 11; Indels 105; Gaps 3;

QY 11 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 70
|||||
Db 1 MDELEDEYNNKTATENNNTAATRNDSFPVWDYKSSVDDLOQYFLIGLYTFVSLGFMGNL 60
QY 71 L1MALMKRRNOKTYVNFILGNLAFSDDLVLVLFCSPTLTSVLLDDQMGKVMCHIMPEL 130
|||||
Db 61 L1MALMKRRNOKTYVNFILGNLAFSDDLVLVLFCSPTLTSVLLDDQMGKVMCHIMPEL 120

Matches 308; Conservative 14; Mismatches 18; Indels 105; Gaps 3;

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